GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 09:49:14 ; Search time 1478 Seconds
(without alignments)
11277.670 Million cell updates/sec

Title: US-10-607-806-1-C7256_COPY_7000_9500
Perfect score: 2499
Sequence: 1 gtcgtgtcactgctgtccag.....tttgagaccagcctggacaa 2501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2498.6	100.0	12174	12	ADI35082	Adi35082 Human PLA
	2	2497.4	99.9	12174	12	ADJ09983	Adj09983 Human pho
	3	2497.4	99.9	13612	6	ABK47376	Abk47376 Human Pho
c	4	456.6	18.3	42360	13	ABD33466	Abd33466 Human can
	5	434.2	17.4	93544	13	ABD33504	Abd33504 Human can
c	6	434.2	17.4	160482	11	ACN43914	Acn43914 Human gen
c	7	433.2	17.3	91760	11	ACN44410	Acn44410 Human gen
c	8	425.4	17.0	38538	13	ABD33357	Abd33357 Human can
	9	417.2	16.7	122888	6	ABK83569	Abk83569 Human cDN
c	10	416.2	16.7	6405	5	AAF97850	Aaf97850 Human neu
c	11	416	16.6	126990	12	ADP13332	Adp13332 Renal cel
c	12	414.2	16.6	196686	11	ACN44170	Acn44170 Human gen
c	13	413.6	16.6	86000	12	ADP68568	Adp68568 Human PPA
c	14	413.6	16.6	215974	12	ADQ97523	Adq97523 Human can
c	15	413.4	16.5	13670	6	AAL42369	Aal42369 Human Gua
	16	413.2	16.5	6519	5	ABA16909	Aba16909 Human ner
	17	408.8	16.4	17245	4	AAK83897	Aak83897 Human imm
	18	406.2	16.3	348101	12	ADQ97146	Adq97146 Human can
c	19	405.8	16.2	227246	13	ABD33272	Abd33272 Human can
c	20	404	16.2	95240	10	ADL13556	Adl13556 Osteoarth
c	21	403.6	16.2	23639	6	ABQ78991	Abq78991 Human pho
c	22	400.4	16.0	14176	4	AAS26670	Aas26670 Human gen
c	23	400.4	16.0	14176	8	ABX74019	Abx74019 Human nov
c	24	400.4	16.0	177531	8	ACF62732	Acf62732 Cancer ba
c	25	400.4	16.0	177531	8	ADB20847	Adb20847 MRP1 base
c	26	400.4	16.0	177531	10	ADB87936	Adb87936 Human UGT
c	27	400.4	16.0	177531	10	ADB96919	Adb96919 Human MDR
c	28	400.4	16.0	177531	10	ADB92110	Adb92110 Human MDR
c	29	400.4	16.0	177531	10	ADH74617	Adh74617 Human BAC
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	38	391.4	15.7	226475	9	AAD58279	Aad58279 Human tum
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	42	390	15.6	36221	4	AAS00624	Aas00624 Human dea
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ALIGNMENTS

RESULT 1
ADI35082
ID ADI35082 standard; DNA; 12174 BP.
XX
AC ADI35082;
XX
DT 22-APR-2004 (first entry)
XX
DE Human PLA2G1B nucleotide sequence.
XX
KW PLA2G1B ; fat deposition; leanness; polymorphism;
KW non-insulin dependent diabetes mellitus; NIDDM; hyperinsulinemia;
KW hypertension; glucose intolerance; dyslipidemia; hypercoagulability;
KW microalbuminuria; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2004002295-A2.
XX
PD 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-US020830.
XX
PR 27-JUN-2002; 2002US-0392361P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Adam GIR, Langdown ML;
XX
DR WPI; 2004-082843/08.
DR P-PSDB; ADI35083.
XX
PT Diagnosing a predisposition to fat deposition or leanness, useful for
PT diagnosing a predisposition to e.g. diabetes or hypertension, comprises
PT detecting the presence of a polymorphism in the PLA2G1B nucleic acid from
PT the subject.
XX
PS Claim 1; SEQ ID NO 1; 91pp; English.
XX
CC The invention relates to diagnosing a predisposition to fat deposition or
CC leanness in a subject comprising detecting the presence or absence of a
CC polymorphic variation associated with fat deposition at a polymorphic

CC site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a
CC subject, where the presence of the polymorphic variation indicates a
CC predisposition to fat deposition in the subject. The polymorphic
CC variation is a guanine at position 7328 or thymine at position 9182 of
CC the present sequence. The method is useful for diagnosing a
CC predisposition to fat deposition or leanness in a subject, and
CC consequently for diagnosing a predisposition to non-insulin dependent
CC diabetes mellitus (NIDDM) in a subject and conditions such as
CC hyperinsulinemia, hypertension, glucose intolerance, dyslipidemia,
CC hypercoagulability, or microalbuminuria, which can lead to early
CC prescription of preventive measures. The present sequence represents a
CC human PLA2G1B nucleotide sequence.
XX
SQ Sequence 12174 BP; 3217 A; 2992 C; 2738 G; 3215 T; 0 U; 12 Other;

Query Match 100.0%; Score 2499; DB 12; Length 12174;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2500; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTCGTGTCACTGCTGTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATG 60
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Db       7000 GTCGTGTCACTGCTGTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATG 7059

Qy         61 CTTTCAATAAATATATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCC 120
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Db       7060 CTTTCAATAAATATATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCC 7119

Qy        121 TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGGCTGAC 180
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Db       7120 TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGGCTGAC 7179

Qy        181 CTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGA 240
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Db       7180 CTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGA 7239

Qy        241 CACATGACAACTGCTACGACCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACA 300
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Qy        301 MMCCGTACACCCACACCTATTCATACTCRTGCTCTGGCTCGGCAATCACCTGTAGCAGTA 360
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Qy        541 GAGGCTCAGAAGGCTGAGCTATTTGCCCAAGATCACACAGCTTGTAAGTGGTGACAGTTT 600
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Qy        601 GGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCAC 660
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Qy        661 AGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACC 720
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Qy        721 TCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAA 780
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Db       7720 TCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAA 7779

Qy        781 ATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTT 840
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Qy         841 CAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATG 900
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Qy         901 TGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAG 960
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Qy         961 GGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAA 1020
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Qy        1021 CCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGC 1080
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Qy        1081 CTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTT 1140
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Qy        1141 TAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG 1200
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Qy        1201 ATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGC 1260
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Db       8380 TTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCA 8439

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Qy       1921 TTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGC 1980
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Qy       2101 AGTTTAAATGCATTTTAACTGTAATCTTATTGTTTATTTTGGTTATAAAAGTAAACAAGC 2160
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Qy       2161 CAAAAGTAATGCAACTTCAAACKCTACATAAATATCTATTATGGAAAGTGGAAGGCATCT 2220
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Qy       2221 ATAATCCTACTACCCAAAGATAACCAGTTACATATTCCTCCAGATTTTTGGGGCATACAC 2280
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Qy       2281 TAGCTTTTTTTATTTGGGAAAATTTCCATGTGCAGGCATACCTAATTTTTCTAAATGTCT 2340
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Qy       2341 ATGTAGTATTCCATTTAAGGATGTTCCATAATTTTTAAAATACATGCTTTAAAGTAGAGA 2400
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RESULT 2
ADJ09983
ID   ADJ09983 standard; DNA; 12174 BP.
XX
AC   ADJ09983;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human phopholipase A2 (PLA2G1B) DNA SeqID 1.
XX
KW   human; gene; ds; fat reduction; fat deposition; phospholipase A2;
KW   PLA2G1B; chromosome 12q24; single nucleotide polymorphism; SNP;
KW   appetite suppressant; lipase inhibitor; exercise regimen; obesity;
KW   non-insulin dependent diabetes mellitus; NIDDM; cardiovascular disorder;
KW   hypertension; antidiabetic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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PF   27-JUN-2003; 2003WO-US020831.
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PR   27-JUN-2002; 2002US-0392362P.
XX
PA   (SEQU-) SEQUENOM INC.
XX
PI   Adam GIR,  Langdown ML,  Denissenko MF,  Dennis E,  Cantor C;
PI   Rubin B;
XX
DR   WPI; 2004-071944/07.
DR   P-PSDB; ADJ09984.
XX
PT   Identifying a candidate therapeutic for fat reduction, useful for
PT   treating diabetes, by introducing a test molecule to a system comprising
PT   PLA2G1B protein or nucleic acid, and determining the presence of
PT   interaction between the compounds.
XX
PS   Claim 1; SEQ ID NO 1; 116pp; English.
XX
CC   This invention relates to a novel candidate therapeutic agent useful for
CC   fat reduction and disorders related to fat depositions. Specifically, it
CC   refers to polymorphic variations in the phospholipase A2 (PLA2G1B) DNA,
CC   which is located on chromosome 12q24 and has been associated with central
CC   fat deposition. The present invention describes methods to detect the
CC   presence or absence of these single nucleotide polymorphisms of PLA2G1B,
CC   in particular G7328A and T9182G, and subsequently provide treatment that
CC   reduces fat deposition. This treatment may consist of an appetite
CC   suppressant, a lipase inhibitor, a phospholipase inhibitor, an exercise
CC   regimen, a dietary regimen, psychological counselling, psychotherapy or a
CC   psychotherapeutic. Accordingly, PLA2G1B is a target for reducing fat
CC   deposition and it can be used to treat both obesity and non-insulin
CC   dependent diabetes mellitus (NIDDM), as well as cardiovascular disorders
CC   such as hypertension. As such, it exhibits antidiabetic activity. This
CC   polynucleotide sequence is the human PLA2G1B DNA of the invention.
XX
SQ   Sequence 12174 BP; 3220 A; 2996 C; 2739 G; 3219 T; 0 U; 0 Other;

  Query Match             99.9%;  Score 2497.4;  DB 12;  Length 12174;
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Best Local Similarity   99.8%;  Pred. No. 0;
Matches 2495;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCGTGTCACTGCTGTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7000 GTCGTGTCACTGCTGTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATG 7059

Qy         61 CTTTCAATAAATATATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCC 120
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Db       7060 CTTTCAATAAATATATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCC 7119

Qy        121 TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGGCTGAC 180
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Db       7120 TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGGCTGAC 7179

Qy        181 CTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGA 240
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Qy        241 CACATGACAACTGCTACGACCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACA 300
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Qy       1201 ATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGC 1260
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Db       8380 TTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCA 8439

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Db       9460 TGGATCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGACAA 9500


RESULT 3
ABK47376
ID   ABK47376 standard; DNA; 13612 BP.
XX
AC   ABK47376;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human Phospholipase A2, groupIB (PLA2G1B) gene.
XX
KW   Human; ds; gene; SNP; single nucleotide polymorphism; pancreatitis;
KW   pancreatic cancer; Phospholipase A2 groupIB; PLA2G1B; gene therapy;
KW   haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  l
FT                   /number= 4
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FT                   /label= SNP
FT                   /note= "Single nucleotide polymorphism"
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PD   14-FEB-2002.
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PF   06-AUG-2001; 2001WO-US024663.
XX
PR   04-AUG-2000; 2000US-0223179P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Kazemi A,  Kliem SE,  Koshy B;
XX
DR   WPI; 2002-303982/34.
DR   P-PSDB; AAU78667.
XX
PT   Novel isolated human Phospholipase A2, Group IB pancreas polynucleotide,
PT   for therapeutic purposes, for studying expression and function of the
PT   polynucleotide and for expressing the phospholipase protein.
XX
PS   Claim 1; Fig 1; 51pp; English.
XX
CC   The invention relates to an isolated human Phospholipase A2, Group IB
CC   (pancreas) (PLA2G1B) polynucleotide comprising a sequence which is a
CC   polymorphic variant for a reference sequence for the PLA2G1B gene or its
CC   fragment, or a polymorphic variant of a reference sequence for a PLA2G1B
CC   cDNA or its fragment. Also included are haplotyping/genotyping the
CC   PLA2G1B gene of an individual, predicting the haplotype pair for the
CC   PLA2G1B gene of an individual, identifying an association between a trait
CC   and at least one haplotype or haplotype pair of the PLA2G1B gene, an
CC   isolated genotyping oligonucleotide for detecting a polymorphism in the
CC   PLA2G1B gene, a recombinant non-human organism transformed or transfected
CC   with the PLA2G1B sequence, where the organism expresses a PLA2G1B protein
CC   encoded by the first nucleotide sequence or by the polymorphic variant
CC   sequence, an isolated polypeptide comprising a sequence which is a
CC   polymorphic variant of a reference sequence for the PLA2G1B protein or
CC   its fragment, an anti-PLA2G1B monoclonal antibody, screening for drugs
CC   targeting PLA2G1B, a computer system for storing and analysing
CC   polymorphism data for the PLA2G1B gene and a genome anthology for PLA2G1B
CC   gene. The PLA2G1B variant is useful in studying the expression and
CC   function of PLA2G1B, and in expressing PLA2G1B protein for use in
CC   screening for candidate drugs to treat diseases related to PLA2G1B
CC   activity (e.g. pancreatitis and pancreatic cancer) and for therapeutic
CC   purposes. The transgenic organism is useful for studying expression of
CC   the PLA2G1B isogenes in vivo, for in vivo screening and testing of drugs
CC   targeted against PLA2G1B protein, and for testing the efficacy of
CC   therapeutic agents and compounds in a biological system. The antibody is
CC   useful for studying the effect of the variation on the biological
CC   activity of PLA2G1B as well as on the binding affinity of candidate drugs
CC   targeting PLA2G1B. The present sequence is the PLA2G1B gene which is
CC   located on chromosome 12q23-q24.1
XX
SQ   Sequence 13612 BP; 3637 A; 3290 C; 3070 G; 3615 T; 0 U; 0 Other;

  Query Match             99.9%;  Score 2497.4;  DB 6;  Length 13612;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2495;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCGTGTCACTGCTGTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATG 60
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Db    6576 CTTTCAATAAATATATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCC 6635

Qy     121 TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGGCTGAC 180
Db    6636 TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGGCTGAC 6695

Qy     181 CTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGA 240
Db    6696 CTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGA 6755

Qy     241 CACATGACAACTGCTACGACCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACA 300
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Db    7176 AGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACC 7235

Qy     721 TCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAA 780
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Qy     781 ATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTT 840
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Db    7356 CAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATG 7415

Qy     901 TGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAG 960
Db    7416 TGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAG 7475

Qy     961 GGATTACTGCCTATTTTCTTCCTTTCTTTTTGAGACAGAGTCTCACTTCATCACCTCAA 1020
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Qy    1021 CCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGC 1080
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Db    7776 CGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATAT 7835

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Db    7836 AGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCTT 7895

Qy    1381 TTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCA 1440
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Db    7956 CTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTTC 8015

Qy    1501 ATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTC 1560
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Qy    1621 TACACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGA 1680
Db    8136 TACACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGA 8195

Qy    1681 AACCTGCATTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGA 1740
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Db    8256 CTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGA 8315

Qy    1801 AGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAAAATT 1860
Db    8316 AGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAAAATT 8375

Qy    1861 AGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAA 1920
Db    8376 AGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAA 8435

Qy    1921 TTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGC 1980
Db    8436 TTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGC 8495

Qy    1981 CTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATAAAGGATCGGAG 2040
Db    8496 CTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATAAAGGATCGGAG 8555

Qy    2041 AGAAACAAAACTAATAAGATTCCTGAAGGTAAGCAGAGATACGTAAATTATATGTAATAA 2100
Db    8556 AGAAACAAAACTAATAAGATTCCTGAAGGTAAGCAGAGATACGTAAATTATATGTAATAA 8615

Qy    2101 AGTTTAAATGCATTTTAACTGTAATCTTATTGTTTATTTTGGTTATAAAAGTAAACAAGC 2160
Db    8616 AGTTTAAATGCATTTTAACTGTAATCTTATTGTTTATTTTGGTTATAAAAGTAAACAAGC 8675

Qy    2161 CAAAAGTAATGCAACTTCAAACKCTACATAAATATCTATTATGGAAAGTGGAAGGCATCT 2220
Db    8676 CAAAAGTAATGCAACTTCAAACTCTACATAAATATCTATTATGGAAAGTGGAAGGCATCT 8735
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Qy       2221 ATAATCCTACTACCCAAAGATAACCAGTTACATATTCCTCCAGATTTTTGGGGCATACAC 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8736 ATAATCCTACTACCCAAAGATAACCAGTTACATATTCCTCCAGATTTTTGGGGCATACAC 8795

Qy       2281 TAGCTTTTTTTATTTGGGAAAATTTCCATGTGCAGGCATACCTAATTTTTCTAAATGTCT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8796 TAGCTTTTTTTATTTGGGAAAATTTCCATGTGCAGGCATACCTAATTTTTCTAAATGTCT 8855

Qy       2341 ATGTAGTATTCCATTTAAGGATGTTCCATAATTTTTAAAATACATGCTTTAAAGTAGAGA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8856 ATGTAGTATTCCATTTAAGGATGTTCCATAATTTTTAAAATACATGCTTTAAAGTAGAGA 8915

Qy       2401 AACTAGGTTGGGCATGGTGGCTCACGCCTGTATCCCAGCACTTTGGGAGGCCGAGGCAAA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8916 AACTAGGTTGGGCATGGTGGCTCACGCCTGTATCCCAGCACTTTGGGAGGCCGAGGCAAA 8975

Qy       2461 TGGATCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGACAA 2501
             |||||||||||||||||||||||||||||||||||||||||
Db       8976 TGGATCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGACAA 9016


RESULT 4
ABD33466/c
ID   ABD33466 standard; DNA; 42360 BP.
XX
AC   ABD33466;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human cancer-associated (CA) gene HD07-089.
XX
KW   Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW   ds; cancer; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004058146-A2.
XX
PD   15-JUL-2004.
XX
PF   15-DEC-2003; 2003WO-US040081.
XX
PR   17-DEC-2002; 2002US-00322281.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2004-499109/47.
XX
PT   Novel human cancer associated protein encoded within open reading frame
PT   of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS   Claim 16; SEQ ID NO 618; 182pp; English.
XX
CC   The invention relates to cancer-associated proteins (CAP) and the cancer-
CC   associated (CA) nucleic acids encoding them. The invention also relates
CC   to a method for treating cancers involving administering to a patient an
CC   inhibitor of CAP, and a method of screening for anticancer activity in a
CC   potential drug involving providing a cell that expresses a CA gene,
CC   contacting a tissue sample derived from a cancer cell with an anticancer
CC   drug candidate and monitoring the effect of the anticancer drug candidate
CC   on expression of the CA gene. The CAP proteins are useful for detecting
CC   cancer associated with expression of a CAP protein in a test cell sample
CC   and for screening for a bioactive agent capable of modulating the
CC   activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC   cancer, involving determining the expression of a CA nucleic acid in a
CC   tissue. This sequence represents a human CA gene of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX

SQ   Sequence 42360 BP; 11698 A; 9658 C; 10445 G; 10559 T; 0 U; 0 Other;

  Query Match             18.3%;  Score 456.6;  DB 13;  Length 42360;
  Best Local Similarity   99.8%;  Pred. No. 4.8e-84;
  Matches  456;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2045 ACAAAACTAATAAGATTCCTGAAGGTAAGCAGAGATACGTAAATTATATGTAATAAAGTT 2104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      42360 ACAAAACTAATAAGATTCCTGAAGGTAAGCAGAGATACGTAAATTATATGTAATAAAGTT 42301

Qy       2105 TAAATGCATTTTAACTGTAATCTTATTGTTTATTTTGGTTATAAAAGTAAACAAGCCAAA 2164
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      42300 TAAATGCATTTTAACTGTAATCTTATTGTTTATTTTGGTTATAAAAGTAAACAAGCCAAA 42241

Qy       2165 AGTAATGCAACTTCAAACKCTACATAAATATCTATTATGGAAAGTGGAAGGCATCTATAA 2224
             ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db      42240 AGTAATGCAACTTCAAACTCTACATAAATATCTATTATGGAAAGTGGAAGGCATCTATAA 42181

Qy       2225 TCCTACTACCCAAAGATAACCAGTTACATATTCCTCCAGATTTTTGGGGCATACACTAGC 2284
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      42180 TCCTACTACCCAAAGATAACCAGTTACATATTCCTCCAGATTTTTGGGGCATACACTAGC 42121

Qy       2285 TTTTTTTATTTGGGAAAATTTCCATGTGCAGGCATACCTAATTTTTCTAAATGTCTATGT 2344
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      42120 TTTTTTTATTTGGGAAAATTTCCATGTGCAGGCATACCTAATTTTTCTAAATGTCTATGT 42061

Qy       2345 AGTATTCCATTTAAGGATGTTCCATAATTTTTAAAATACATGCTTTAAAGTAGAGAAACT 2404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      42060 AGTATTCCATTTAAGGATGTTCCATAATTTTTAAAATACATGCTTTAAAGTAGAGAAACT 42001

Qy       2405 AGGTTGGGCATGGTGGCTCACGCCTGTATCCCAGCACTTTGGGAGGCCGAGGCAAATGGA 2464
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      42000 AGGTTGGGCATGGTGGCTCACGCCTGTATCCCAGCACTTTGGGAGGCCGAGGCAAATGGA 41941

Qy       2465 TCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGACAA 2501
             |||||||||||||||||||||||||||||||||||||
Db      41940 TCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGACAA 41904


RESULT 5
ABD33504
ID   ABD33504 standard; DNA; 93544 BP.
XX
AC   ABD33504;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human cancer-associated (CA) gene HD07-098.
XX
KW   Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW   ds; cancer; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004058146-A2.
XX
PD   15-JUL-2004.
XX
PF   15-DEC-2003; 2003WO-US040081.
XX
PR   17-DEC-2002; 2002US-00322281.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2004-499109/47.
XX
PT   Novel human cancer associated protein encoded within open reading frame
PT   of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS   Claim 16; SEQ ID NO 676; 182pp; English.
XX
```

```
CC   The invention relates to cancer-associated proteins (CAP) and the cancer-
CC   associated (CA) nucleic acids encoding them. The invention also relates
CC   to a method for treating cancers involving administering to a patient an
CC   inhibitor of CAP, and a method of screening for anticancer activity in a
CC   potential drug involving providing a cell that expresses a CA gene,
CC   contacting a tissue sample derived from a cancer cell with an anticancer
CC   drug candidate and monitoring the effect of the anticancer drug candidate
CC   on expression of the CA gene. The CAP proteins are useful for detecting
CC   cancer associated with expression of a CAP protein in a test cell sample
CC   and for screening for a bioactive agent capable of modulating the
CC   activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC   cancer, involving determining the expression of a CA nucleic acid in a
CC   tissue. This sequence represents a human CA gene of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 93544 BP; 26138 A; 20027 C; 21635 G; 25744 T; 0 U; 0 Other;

  Query Match             17.4%;  Score 434.2;  DB 13;  Length 93544;
  Best Local Similarity   59.7%;  Pred. No. 2.4e-79;
  Matches  861;  Conservative    1;  Mismatches  559;  Indels   22;  Gaps    7;

Qy        604 TTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGT 663
Db      18099 TTTTTTTTTTTTTTTTTTGAGAGATGGAGTCTTAGCCTGTTGCCCAGGCTGGAGTGCAGT 18158

Qy        664 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 723
Db      18159 GGCACCATCTTGGGTCACTGCAACCTCCACCATGTGGGTTCAAGAGATTCTACTGCCTCA 18218

Qy        724 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATT 783
Db      18219 ACCTCCCAAGTAGCTGGAATTACAGGCTTGTGCCACCACACCTTGCTAATT--TTTGTGT 18276

Qy        784 TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAA 843
Db      18277 TTTTATTAGAGACAGGGTTTCGCCATGTTGGCCAGGCTGATCTCAAACTCCTGGCCTCAA 18336

Qy        844 GCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 903
Db      18337 CTGATCCGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAAGTGTGAGCCACCATGCCT 18396

Qy        904 GGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGA 963
Db      18397 GGCCACCACAGGCTTTATTTACAGGTTGCCTCATTACCTGAATTCTCTCTCTCCAAATTC 18456

Qy        964 TTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCA---A 1020
Db      18457 TTGTTACCCAAACACAGGAACATGAGATGGAGTCTCGCTCCGTCGCCCAGTCTGGAGTGC 18516

Qy       1021 CCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGC 1080
Db      18517 AGTGATCTCAGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGTGATTCTTCTGCCTCAGC 18576

Qy       1081 CTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTT 1140
Db      18577 CTCCCAAGTAGCTGGGACTACAGGCATGCGCCACCCCACCTGGCTAA-TTTTTGTATTTT 18635

Qy       1141 TAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG 1200
Db      18636 TAGTAGAGACGGGGTTTCACCATGCTGGCCAGGCTGGTCTCGAACTCCTGACCTC--GTG 18693

Qy       1201 ATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGC 1260
Db      18694 ATCCACCCGCCTCAGCTTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCATACCTGGC 18753

Qy       1261 CGATTACTGTCTATTTT------CTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTG 1314
Db      18754 CAGGAACTAGACAGTTTTAGAGACATCTTTCTGAAATAGGGCTGGTGCCCCTCATTATTC 18813

Qy       1315 ACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTT 1374
Db      18814 ATTAATGCTATTTTCTCCAAAACCCGGGAACCAAATAGATGTGATAGCATGGCATCCCTC 18873

Qy       1375 TTTCTTTTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCT 1434
Db      18874 ATGATCTGAAGTTACTGTCCGTAACTGCGGTCCCATTCGATTTGGATATTGGGGGATGCC 18933

Qy       1435 TTTTCACTTATCA-CCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTATTGTTACTG 1493
Db      18934 TGCACGTGTCTGTGTCATGTGCTGCATGTCTGCGGTGCCATCAGTCTGTGAGCTCCCTCT 18993

Qy       1494 TTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCT 1553
Db      18994 GGGCCTGCGTCCGTTTTTCTCATCCTTTGTATTATCTCAGCACTTTGTACAATACCTGGC 19053

Qy       1554 CCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCC 1613
Db      19054 ACTCAATGAATTAAAAATAATCTGAAGCGGGGGTTGGGGGGAGCTTGTCAATATAGCCCC 19113

Qy       1614 AGAGAAATACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAA 1673
Db      19114 ACCTTGTTTTGCCCTTGGACTTGATAAAGCCGTTTGTTGCTATGCATATGTCCATCTCTT 19173

Qy       1674 GACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCA------- 1726
Db      19174 TTCTAGACAATGAGTTACTTGGATGAATAGGCAGATCTCTTGGTTAAACCATAAAGACAG 19233

Qy       1727 GTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGAT 1786
Db      19234 GCTGGGCGCGGTGGCTCACATCTGTAATCCCAGCACTTTGAGAGGCCGAGGCGGGCAGAT 19293

Qy       1787 CACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTA 1846
Db      19294 CACTTGAGGTTAGAAGTTCGATACCAGCCTGGCCAACATGGTGAAACCCAATCTCTACTA 19353

Qy       1847 AAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGG 1906
Db      19354 AAAATACAAAAATTAGCCGAGTGCGGTGGCGCATGCCTGTAATCCTAGCTACTTGGGAGG 19413

Qy       1907 CTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCAC 1966
Db      19414 CTGAGGCAGGAGAATCGCTTGAACCCGGGAGGTGAAGCTTTCAGTGAGCCGAGATTGTGC 19473

Qy       1967 CACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAA 2026
Db      19474 CATTACACTCCAGCCTGGGCAACAGAGCGAGACTGTGTCTCAAAATGAAAACCCATAAAG 19533

Qy       2027 ATA 2029
Db      19534 ACA 19536


RESULT 6
ACN43914/c
ID   ACN43914 standard; DNA; 160482 BP.
XX
AC   ACN43914;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human genomic sequence hCG26773.
XX
KW   Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003073826-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006235.
XX
PR   01-MAR-2002; 2002US-00087192.
XX
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PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW;
XX
DR   WPI; 2003-328604/31.
XX
PT   Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT   comprises a nucleotide sequence.
XX
PS   Claim 1; SEQ ID NO 100; 0pp; English.
XX
CC   The present invention relates to novel DNA and protein sequences which
CC   are associated with carcinomas. The sequences are useful for: (i) for
CC   screening drug candidates; (ii) for screening of bioactive agent capable
CC   of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC   a bioactive agent capable of modulating the activity of CAP; (iv) for
CC   evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC   carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC   carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC   (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC   determining Carcinoma Associated (CA) gene copy number. In addition, the
CC   CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC   carcinoma including lymphoma. The present sequence is one such CA coding
CC   sequence. Note: This patent is an equivalent to basic patent
CC   US2002182586A1, for which no sequence data was published
XX
SQ   Sequence 160482 BP; 44060 A; 32143 C; 33530 G; 49875 T; 0 U; 874 Other;

  Query Match             17.4%;  Score 434.2;  DB 11;  Length 160482;
  Best Local Similarity   60.2%;  Pred. No. 2.7e-79;
  Matches  888;  Conservative    1;  Mismatches  525;  Indels   61;  Gaps    8;

Qy        606 TTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTGG 665
Db       5181 TGTTTTTTTTTTTCTCTCGATACGGAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGG 5122

Qy        666 TGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGC 725
Db       5121 CATGATCTCGGCTCACTGAAACCTCTGCCTCCTGGGTTCACGTGATTCTCCTGCCTCAGA 5062

Qy        726 CTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGG--CTAATTAAAAAAATT 783
Db       5061 CTCCCAAGTAGCTGGGATTACAGGCGTGAGCCACCATGCCTGGCCCTAATGTTTTGTATT 5002

Qy        784 TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAA 843
Db       5001 TTTTAGTAGAGAC-AGGTTTCGCTACATTGGTCAGGCTAGTCTCAAACTCCTGACCTCAA 4943

Qy        844 GCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 903
Db       4942 GTGATCCGCCTGCCTTGATGTACCAAAGTGCTGGGATTACAGATGTGAGCCACCCCGCCC 4883

Qy        904 GGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGA 963
Db       4882 GGCCAGTCATTCACTTTCTTTCTTTTTTTTTTTTTTTTGAGACAGAGTCTCATTCTGTC 4823

Qy        964 TTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCT 1023
Db       4822 ATCCAGGCTGGAGTGT----------------------------------AGTGGCAC 4799

Qy       1024 CCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTC 1083
Db       4798 GATCTCGGCTCACTTCAACTTTCACCTCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTC 4739

Qy       1084 CTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTTTAG 1143
Db       4738 TTGAGTAGCTGGGATTACAGGCATGCACCACCGCACCCGGCTAATTTTTTATATTTTTGG 4679

Qy       1144 CAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC 1203
Db       4678 GAGAGATGGGGTTTCACCATGTTAGACAGGCTGGTCTCAAACTCCTGACCTCAAGCAATC 4619

Qy       1204 TGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCGA 1263
Db       4618 TGCTCGCCTTGGCCTCCTAAAGTGCTGGGATTACAGGCGTGAGCCACCACACCCGGCCAA 4559

Qy       1264 TTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGT 1323
Db       4558 --ATCATTCACTTTCTACAACAAGTTCTGTCTGTATGCCAATGAATCTCAGGACTGTACT 4501

Qy       1324 AGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCTTTTT 1383
Db       4500 TCTAGCTCTAACCTCTAAACATATATTTAAGTGTCCTTTAAAGCCAGGACTTAGATTCCT 4441

Qy       1384 TTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCACTT 1443
Db       4440 CAGAATCTCAAATTCAACAAATCCAAAATTCAACATATATTTTCCCTAAATTCTGCCCCT 4381

Qy       1444 ATCACCTTGTTA------TGACTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTT 1497
Db       4380 TTCTCTGTATTTCCTAGTTTGCTTAATAGTATCACCTTAATTCAAGGAAGAAATTTCAAA 4321

Qy       1498 TTCATTGTTACTATTTTAGTCACTGAAT--AATATGGCTTAATTTGCTTATACATCCTCC 1555
Db       4320 GTCATCTTCAATTTTTCTCTCTCTCAACGCAATAAAGCACTAATTCCTAGAAGCTCAACC 4261

Qy       1556 TGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAG 1615
Db       4260 TTAAACAGTCCTCTGGAATGAGATGAAGGTTAACAGTTACTGAACACAGACCAAAACTAG 4201

Qy       1616 AGAAATACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGA 1675
Db       4200 GCACAGCAGCAAGGGTTGTTCAATTGAATTCAATTCTCTCAGAAGCCCTAAGGAATAGCT 4141

Qy       1676 CAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAAAAAT------AACTCAGTT 1729
Db       4140 CCAATTTTATAGAGGAAGAAACTGAGGTTCCAAGAAGTAAGAAATTCACACAAGGAGGCT 4081

Qy       1730 GGGCACAGTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCAC 1789
Db       4080 GGGTGTGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGCAGATCAC 4021

Qy       1790 TTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAA 1849
Db       4020 CTGAGGTCAAGAGCTCGAGACCAGCCTGACAAACATGGTGAAACCCCATCTCTACTAAAA 3961

Qy       1850 ATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTG 1909
Db       3960 ATACAAAAATTACCCAGGTGTGGTGGTGCACGCCTGTAATCCCAGCTATTTGGGAGGCTG 3901

Qy       1910 AGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCC------GAGATCC 1963
Db       3900 ACGCAGGAGAATTGTTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCAAGATGGAGATCG 3841

Qy       1964 CACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAAT 2023
Db       3840 TGCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCTGTCTCCAAAAAAAAAAAAAAA 3781

Qy       2024 AAAATAAAGGATCGGAGAGAAACAAAACTAATAAG 2058
Db       3780 AGAAAGAAAGAAAGAAAAAAATAAATTCACACAAG 3746


RESULT 7
ACN44410/c
ID   ACN44410 standard; DNA; 91760 BP.
XX
AC   ACN44410;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human genomic sequence hCG41365.
XX
KW   Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS   Homo sapiens.
```

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XX
PN   WO2003073826-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006235.
XX
PR   01-MAR-2002; 2002US-00087192.
XX
PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW;
XX
DR   WPI; 2003-328604/31.
XX
PT   Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT   comprises a nucleotide sequence.
XX
PS   Claim 1; SEQ ID NO 844; 0pp; English.
XX
CC   The present invention relates to novel DNA and protein sequences which
CC   are associated with carcinomas. The sequences are useful for: (i) for
CC   screening drug candidates; (ii) for screening of bioactive agent capable
CC   of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC   a bioactive agent capable of modulating the activity of CAP; (iv) for
CC   evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC   carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC   carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC   (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC   determining Carcinoma Associated (CA) gene copy number. In addition, the
CC   CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC   carcinoma including lymphoma. The present sequence is one such CA coding
CC   sequence. Note: This patent is an equivalent to basic patent
CC   US20021825864A1, for which no sequence data was published
XX
SQ   Sequence 91760 BP; 21177 A; 23589 C; 24129 G; 22845 T; 0 U; 20 Other;

  Query Match             17.3%;  Score 433.2;  DB 11;  Length 91760;
  Best Local Similarity   61.6%;  Pred. No. 3.8e-79;
  Matches  906;  Conservative    1;  Mismatches  474;  Indels   89;  Gaps   10;

Qy        606 TTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTGG 665
Db       5566 TTTTTTTGTTTTAAATTAGAGACTGGGTTTTGCTCTGTCGCCCAGGATGGAGTACAGTGG 5507

Qy        666 TGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGC 725
Db       5506 CATGATCATGGCTCACTACAACCTCTGCCTCCTGGGCTCAGGCAATCCTCCCACCTCAGC 5447

Qy        726 CTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAAT-TT 784
Db       5446 CT-CCGAGTAGCTGGAACTACAGGTGAGCACCACCACACCTGGCTAATTTATTTTTTATT 5388

Qy        785 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAG 844
Db       5387 TGTTGTTGAGAGAGGGTCTCGCTATGT------GGCTGGTCTTGAACTCCTGGGCTCAAG 5334

Qy        845 CAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCG 904
Db       5333 TGATCCTCCCACCTCGGCCTCTCAAAGCGCTGGGATTCCAGGTGTCAGCCTCTACACCCA 5274

Qy        905 GCTACTTATTTCTTT----------------------------ACATTCCATCTTTCC 934
Db       5273 GCTCATAAATACTTTTTAAATACCCAGATAATCTTGCTGCTGGCCAAAGAACAAACTTTT 5214

Qy        935 AATAGAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGA 994
Db       5213 ACTTGCTCCCCAAATCTAAAGAATAGTGACTATAG---ACTTGATTTTCTTTTTTTTTAA 5157

Qy        995 GACAGAGTCTCACTTCATCACCTCAACCTCCGTTCAG--------------CTCACTGCA 1040
Db       5156 GGTGGAGTATTGTTCTGTCGCCTAGGCTTGAGTGCAGTGGTGTGATCTTGACTCACTGCA 5097

Qy       1041 ACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTA 1100
Db       5096 ACCTCCTCCTTCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCAGAGTAGCTGGGACTG 5037

Qy       1101 CAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTTTAGCAGAGATGGGGTTTTAC 1160
Db       5036 CAGGTGCGCTCCACCACGCCCAGCTAATTTTTTATATTTTTAGTAGAGATGGGGTTTCAC 4977

Qy       1161 CATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCC 1220
Db       4976 CACTTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAAGTGATCCACCTGCCTCGACCTCC 4917

Qy       1221 CAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTT 1280
Db       4916 CAAAGCGCTGGGATTATAGGCATGAGCCAATGCATCTGGCTGAAAGGATAAATTCTTCTC 4857

Qy       1281 TATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAA 1340
Db       4856 TTTTTTAGCATTTTCTTCTGGTCATTACAGCCA------------TGCTGGTACATACA 4810

Qy       1341 TTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCTTTTTTTAAAACAATCTTGACA 1400
Db       4809 TGTTTTTCTGGCTGATTTTGACCTGTGACTTTCTTTTCTTCTTCTTCTTTCTTCTTCTCT 4750

Qy       1401 ACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCACTTATCACCTTGTTATGACT 1460
Db       4749 CTTCTTCTTCTT--CCTCCTCCTTCTTCTTCTCCTCTTCCTCCTCTTCCTTCTTCTT 4692

Qy       1461 TTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTCAC 1520
Db       4691 TTCTTCTTCTTTCTTCTTCTTTTCTTTTCTCCTTCTTCTCCTCCTTCCTCTTCTCCTCTC 4632

Qy       1521 TGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTT 1580
Db       4631 CTTCCTCTTTTCCTTCCTCTCCTTCCTCTCTTTCCTCTCCCACCT------------CTC 4584

Qy       1581 ACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGAGAAATACACACACACACACACACT 1640
Db       4583 CCTCCTCTCCCTCTTCCTCTTCTTCCTCTTCCTCCTCTTCTTCTTCCTTCCTCTTCCTCT 4524

Qy       1641 CACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTT 1700
Db       4523 TCTTCTCTTTCTTCTTTCTCCTCCTCCTCCT-------TGTTCTTCTTTTCTTTTCTTTT 4471

Qy       1701 TGTTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGT 1760
Db       4470 CTTTTCTTTTTTAAATATAGAGACAGGCCAGGTGCGGTGGCTGACGCCTGTAATCCCAAC 4411

Qy       1761 ACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTC 1820
Db       4410 ACTTTGGGAGGCCAAGGCGGGCGGATCACTTGAGGTCAGCAGTTCAAGACCAGCCTGGCC 4351

Qy       1821 AATATGGTGAAACCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCAT 1880
Db       4350 AACATGGTGAAACTCGGTCTCTACTAAAAATATAAAAATTAGCTGGGTGTGGTGGTGGGT 4291

Qy       1881 GCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCA 1940
Db       4290 GCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCCCTTGAACCCAGGAGGCG 4231

Qy       1941 GAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGGCGACACAGCGAGACT 2000
Db       4230 GAGGTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAGCCTGGGATATATAGAGAGAAT 4171

Qy       2001 CTATCTCAAAAAAATAAATAAATAAAATAA 2030
Db       4170 CCATCTCAAATAAATAAATAAATAAATAAA 4141


RESULT 8
ABD33357/c
ID   ABD33357 standard; DNA; 38538 BP.
XX
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AC   ABD33357;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human cancer-associated (CA) gene HD07-065.
XX
KW   Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW   ds; cancer; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004058146-A2.
XX
PD   15-JUL-2004.
XX
PF   15-DEC-2003; 2003WO-US040081.
XX
PR   17-DEC-2002; 2002US-00322281.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2004-499109/47.
XX
PT   Novel human cancer associated protein encoded within open reading frame
PT   of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS   Claim 16; SEQ ID NO 448; 182pp; English.
XX
CC   The invention relates to cancer-associated proteins (CAP) and the cancer-
CC   associated (CA) nucleic acids encoding them. The invention also relates
CC   to a method for treating cancers involving administering to a patient an
CC   inhibitor of CAP, and a method of screening for anticancer activity in a
CC   potential drug involving providing a cell that expresses a CA gene,
CC   contacting a tissue sample derived from a cancer cell with an anticancer
CC   drug candidate and monitoring the effect of the anticancer drug candidate
CC   on expression of the CA gene. The CAP proteins are useful for detecting
CC   cancer associated with expression of a CAP protein in a test cell sample
CC   and for screening for a bioactive agent capable of modulating the
CC   activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC   cancer, involving determining the expression of a CA nucleic acid in a
CC   tissue. This sequence represents a human CA gene of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 38538 BP; 9418 A; 9893 C; 9523 G; 9684 T; 0 U; 20 Other;

  Query Match             17.0%;  Score 425.4;  DB 13;  Length 38538;
  Best Local Similarity   60.0%;  Pred. No. 1.3e-77;
  Matches  879;  Conservative    1;  Mismatches  552;  Indels   33;  Gaps    9;

Qy        567 CCAAGATCACACAGCTTGTAAGTGGTGACAGTTTGGGTTTTTTTTTGTTGTTGTTTAGAG 626
Db      35304 CAAAAAATAAAAATTAAATATTTTTTGTTTCTTAGATTATAGTTAAGGGGCTTTTTTGAG 35245

Qy        627 ACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCA 685
Db      35244 ATGAAGTTTTGCTCTTGTTGCCCAGGCTGGAGTGCAATGGTGTGATCTTGGCTCACAGCA 35185

Qy        686 GCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTA 745
Db      35184 ACCTCCACCTCCAGGGTTCAAGCGATTCTCCTCTCTCAGCCTCCTGAGTAGCTGGGATTA 35125

Qy        746 CGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATTTTTTTGTAGAGACTGGGTCTTA 805
Db      35124 CAGGCATGCGCCACCACACCCAGCTAATTTTGTA---TTTTTAGTAGAGATGGGGTTTCT 35068

Qy        806 CTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATC 865
Db      35067 CCATGTTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCTCCTTGGCTTC 35008

Qy        866 CCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTC 925
Db      35007 CCGAAGTGTTGGGATTACAGGCATGAGCCACTGCGCCTGGC------CTCAGTTAAGGGA 34954

Qy        926 CATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTT 985
Db      34953 CTTTTTACATATTTATTTATTTATTTATTTATTATTATTTTGAGACGAAGTCTCGCTGTT 34894

Qy        986 CTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTCAGCTCACTGCAACCTC 1045
Db      34893 GTTCTCCAGGCTGGAGTGCAATGGCACGACC-----------TTGGCTCACTGCAACCTC 34845

Qy       1046 TGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGC 1105
Db      34844 CGCCTCCCGGGTTCAAGCGATTCTCCTGTCTTGGCCTCCCAAGTAGCTGGGATTACAGGC 34785

Qy       1106 GTGCACCACCATGCTTGGCTAATTTTTTGTATTTTTAGCAGAGATGGGGTTTTACCATGT 1165
Db      34784 GCCTGCCATCATGCCTGGCTAA-TTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATTA 34726

Qy       1166 TGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAG 1225
Db      34725 TGGCCAGGCTGGTCTTGAAGTCCTGACTTCAGGTGATCTGCCTGCCTCGGCCTCCCAAAG 34666

Qy       1226 TGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTATTG 1285
Db      34665 TGCTGGGATGACAGGTGTGAGCCACCACACTCGGCCTTTATTTATTATTTTCGAGACAGG 34606

Qy       1286 CTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGAT 1345
Db      34605 GTATCTC------TCTGTTGCCCAGGCTGGAGTGCAGTGGTGCAGTCACGGCTGGTTGCA 34552

Qy       1346 GAATGCACAGCCTAGATATAAACTTTCTTTTTCTTTTTTTAAAACAATCTTGACAACTTT 1405
Db      34551 GCCTCAAACTCCTGGGCTCCAGCA--ATTCTCCTGCCTCAGCCTCCTGGGTAGCTGGAAC 34494

Qy       1406 GCAGAATAAATACAATCTTGCATTCTGCTTTTTCACTTATCACCTTGTTATGACTTTTTC 1465
Db      34493 TACAGGTGCAAATTATCATGCCTGGCTAATTTTTAAATTTTTTGTCAAGATGGGGTCTCT 34434

Qy       1466 ATATTGCCTCAAACCTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAAT 1525
Db      34433 CTATATTGCCCAGGCTGGTCTCAAACTCCTGGCCTCAAGTGATCTCCCTTCTGGGCTTCA 34374

Qy       1526 AATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAA 1585
Db      34373 AAAAGTGCTGGGATTATAAGTATGAGCCACCACCTCCGGCCTTCCCTCCTTCCTTCCTTC 34314

Qy       1586 TCTGATGAAAGCTATGAACCCTCTCCCCAGAGAAATACACACACACACACACTCACAC 1645
Db      34313 CTTTCTGCCTTCCTTCCTTCCTTTCTCAAAAAAAAAAAAAAAAGAAGTCAGTGTTGTCTGA 34254

Qy       1646 ACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTC 1705
Db      34253 CTGGTATTGTCTGATTACCTGCATATATTGATATATTATTCCAATAAAGATGCTTGCTTT 34194

Qy       1706 ATA--TTAATTAAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACT 1763
Db      34193 TTCCTTTGGTTAAAAAGTATCCGGCCAGGCGCGATGGCTCACGCTTGTAACCCCAGTACT 34134

Qy       1764 TTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAAT 1823
Db      34133 TTGGGAGGCTGTGGTGGGCGGATCACCTGAGATCAGGAGTACGAGACCAGCCTGGCCAAC 34074

Qy       1824 ATGGTGAAACCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCC 1883
Db      34073 ATGGTAAAACCCCATCTCTACTAGAAATACAAAAATTAGCTGAGTGTAGTGGCACGCACC 34014

Qy       1884 TGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAG 1943
Db      34013 TGTAATCCCAGCTACTTGGGAGGCCAAGGGAGAAGAATTGTTTGAACCCGGGAGGCAGAG 33954

Qy       1944 GTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTA 2003
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                ||||||||||||| ||||| ||||| |||||||||||| |||||||| || ||||||||
Db      33953 GTTGCAGTGAGCCAAGATCACACCATTGCACTCCAGCCAGGGCGACA-AGAGAGACTCTG 33895

Qy       2004 TCTCAAAAAAAATAAATAAATAAAAT 2028
              |||||||||| ||| ||| |  ||
Db      33894 TCTCAAAAAAAAAAAAAAAAAGCAT 33870


RESULT 9
ABK83569
ID   ABK83569 standard; cDNA; 122888 BP.
XX
AC   ABK83569;
XX
DT   14-AUG-2002  (first entry)
XX
DE   Human cDNA differentially expressed in granulocytic cells #140.
XX
KW   Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW   viral infection; parasitic infection; protozoal infection;
KW   fungal infection; sterile inflammatory disease; psoriasis;
KW   rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW   cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW   adult respiratory distress syndrome; inflammatory bowel disease;
KW   Crohn's disease; ulcerative colitis; periodontal disease;
KW   granulocyte activation; chronic inflammation; allergy.
XX
OS   Homo sapiens.
XX
PN   WO200228999-A2.
XX
PD   11-APR-2002.
XX
PF   03-OCT-2001; 2001WO-US030821.
XX
PR   03-OCT-2000; 2000US-0237189P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Beazer-Barclay Y,  Weissman SM,  Yamaga S,  Vockley J;
XX
DR   WPI; 2002-435328/46.
XX
PT   Detecting granulocyte activation by detecting differential expression of
PT   genes associated with granulocyte activation, which serves as diagnostic
PT   markers that is useful for monitoring disease states and drug toxicity.
XX
PS   Claim 1; SEQ ID NO 140; 114pp; English.
XX
CC   The invention relates to detecting (M1) granulocyte (GC) activation
CC   (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC   DNA chip analysis as given in the specification, and comparing the
CC   expression level to an expression level in an unactivated GC, where
CC   differential expression of Gs is indicative of GCA. Also included are
CC   modulating (M2) GA by contacting GC with an agent that alters the
CC   expression of at least one gene in Gs; (2) screening (M3) for an agent
CC   capable of modulating GCA or an inflammation (especially chronic) in a
CC   tissue, an allergic response in a subject, exposure of a subject to a
CC   pathogen or sterile inflammatory disease using the gene expression
CC   profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC   tissue, an allergic response in a subject, exposure of a subject to a
CC   pathogen or sterile inflammatory disease, by detecting the level of
CC   expression in a sample of the tissue of gene(s) from Gs, where the level
CC   of expression of the gene is indicative of inflammation; (4) treating
CC   (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC   response in a subject, exposure of a subject to a pathogen or sterile
CC   inflammatory disease, by contacting a tissue having inflammation with an
CC   agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC   is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC   for screening an agent capable of modulating GCA preferably in an
CC   inflammation in a tissue; M4 is useful for detecting an inflammation
CC   (especially chronic) in a tissue, an allergic response in a subject,
CC   exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC   psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC   cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC   respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC   disease, ulcerative colitis, periodontal disease; also bacterial
CC   infection, viral infection, parasitic infection, protozoal infection,
CC   fungal infection and M5 is useful for treating one of the above
CC   conditions. The present sequence represents a gene differentially
CC   expressed in granulocytes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 122888 BP; 28761 A; 33410 C; 31919 G; 28798 T; 0 U; 0 Other;

  Query Match             16.7%;  Score 417.2;  DB 6;  Length 122888;
  Best Local Similarity   61.1%;  Pred. No. 8.1e-76;
  Matches  894;  Conservative    0;  Mismatches  503;  Indels   65;  Gaps   11;

Qy        604 TTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGT 663
              ||| |||||  | || || | | |||||  |||||| |||||||||||  |||  ||||
Db      70248 TTTCTTTTTTATTTTTTTAACACACAGGTCCTTGCTTTGTCACCCAGGCTGGAGTGCAGT 70307

Qy        664 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 723
              ||||||| || || | || ||| |||||| | |||| |||||||  |||     ||||||
Db      70308 GGTGCAAACACAGCTGACAGCAACCTCAAAC-CCTGGGCTCAAGCAATCCTTCCACCTCA 70366

Qy        724 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAA---------- 772
              || ||||||| ||||||||||||  || ||   ||||| |||  |||||
Db      70367 GCTTCCCAAGAAGCTGGGACTACAGGCATGTGACACCATGCCCAGCTAATTTTTTTTTTT 70426

Qy        773 -----TTAAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTT 827
                  ||  ||||||||||||     |    | |||| ||||  |||  |||||  ||||
Db      70427 TTTACTTTTAAAAATTTTTTGTAGAAATGGGAGTCTCACTATATTGCTTAGGCTGGTCTC 70486

Qy        828 AAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGG 887
              ||| || |||  | |||||||||||||| ||| ||| |||||||||  |||||||| |||
Db      70487 AAATTCTTGGGCTTAAGCAATCCTCCTGCCTCGGCCTCCCAAAGTTGTGGGATTATAGGT 70546

Qy        888 GTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAG 947
              |||    ||||      | |  | |   | | ||   |       |   ||||| || |  |
Db      70547 GTG----ACCACTGCAGCCAGCCTTAATTTCTAATATGGTAAGTATTAATAGCATTTTGG 70602

Qy        948 ATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCAC 1007
                |  || |         | | | || |||  |||||||||||  | ||||  |
Db      70603 GGATGCTCAATAAT-----TTTCTTCTTCTTTTTTTTTTTTTTTGAGATGGGGTCTAGC 70657

Qy       1008 TTCATCACCTCAACCTCCG--------------TTCAGCTCACTGCAACCTCTGCCTCCC 1053
                ||||||  ||    |                |||||  ||||||||||||||||||||
Db      70658 ACTGTCACCTAGACTGGAGTGCAATGGCGCGATTTCAGTTCACTGCAACCTCTGCCTCCT 70717

Qy       1054 GGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCA 1113
              |||||||| |||||| ||||| |||||||||||||||| | |||| ||   | |||
Db      70718 GGGTTCAAGAGATTCTCGTGCCTCAGCCTCCTGAGTAGCTGGGACTACAGGCACCCGCCA 70777

Qy       1114 CCATGCTTGGCTAATTTTTTGTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGG 1173
              |||     |||||||||||||||||||||| |||||| ||||||  | ||||||  |||||
Db      70778 CCACATCCGGCTAATTTTTTGTATTTTTAGTAGAGATAGGGTTTCGCTATGTTGGCCAGG 70837

Qy       1174 CTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAA 1233
              |||||||||||||||||||||  |||||| | ||||||||| ||||||||||||||| |
Db      70838 CTGGTCTCAAACTCCTGACCTC--GTGATCCGACTGCCTCAGCCTCCCAAAGTGCTGGGA 70895

Qy       1234 TTATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCC 1293
              ||| ||| ||||| |||     |  ||          | ||  | |||   | ||||
Db      70896 TTACAGGTGTGAGCCACCACACTCGG-----------CAATAATTTTTTAAGGTATAAAA 70944

Qy       1294 CCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCAC 1353
                  ||| ||          | |       |    | |||| |||| ||||        |
Db      70945 ATGTCCAGAGACCAAAAAGGTCAAGAACCACTGCTTTAAATACATAAATGAT-----ATC 70999

Qy       1354 AGCCTAGATATAAACTTTCTTTTTCTTTTTTTAAAACAATCTTGACAACTTTGCAGAATA 1413
              |  |||  ||||   ||||     |   |||| |||| | ||   |||        ||  |
Db      71000 AAACTATTTATATTATTTCAAAATTACTTTTAAAAAAATTCAACACAGAGCATAAG-CTC 71058
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Qy       1414 AATACAATCTTGCATTCTGCTTTTTCACTTATCACCTTGTTATGACTTTTTCATATTGCC 1473
Db      71059 CATGAAGCAGAGGTTTTTCTTTTTGTTTTATTCATTATGGAAACTAAGTCCCTAGAACAA 71118

Qy       1474 TCAAACCTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGC 1533
Db      71119 TGCCTGGAACATAGTGGGTGTTCAATAAATACTGATTGAATGAATAAAGAATTATATTTT 71178

Qy       1534 TTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGA 1593
Db      71179 GGGTTTTACCCATTCTGATACGTGGACCTCAAACTCATTCTGCTGTTCAGTATTCTATTA 71238

Qy       1594 AAGCTATGAACCCTCTCCCCAGAGAAATACACACACACACACACACTCACACACAGTTTT 1653
Db      71239 TTCCTGAAGATGAAAATATCACAATAACAATTCTATTAATGAACATTTGTTCATAATTTT 71298

Qy       1654 TTTTTAA----TGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATAT 1709
Db      71299 TCATGGACATTTTTATACACAGGTAAGAGTTTCTCCAGGGTATATACCTAAGAATGAAAC 71358

Qy       1710 TAATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACTTTGGAA 1769
Db      71359 TGTAGTAAATAAATCTGGCCAGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGA 71418

Qy       1770 GTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTG 1829
Db      71419 GGCCGAGGCAAGTGGATCAC--AAGGTCAGGGGATCAAGACCATCCTGGCCAACATGGTG 71476

Qy       1830 AAACCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGT 1889
Db      71477 AAACCCTGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGGGGCGTGTGCCTGTAGT 71536

Qy       1890 CCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCA 1949
Db      71537 CCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCGTTTGAACCCAGGAGGTGGAGGTTGCA 71596

Qy       1950 GTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAA 2009
Db      71597 GTGAGCCAAGATCGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAC 71656

Qy       2010 AAAAATAAATAAATAAAATAAA 2031
Db      71657 AAACCAAAAAGAAAAAAAAAAA 71678
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RESULT 10
AAF97850/c
ID AAF97850 standard; DNA; 6405 BP.
XX
AC AAF97850;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:64.
XX
KW Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer;
KW tumour suppressor; human 1p36 homozygosity deletion domain; tumour;
KW diagnosis; ds.
XX
OS Homo sapiens.
XX
PN WO200116311-A1.
XX
PD 08-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-JP005930.
XX
PR 31-AUG-1999; 99JP-00245962.
PR 09-MAY-2000; 2000JP-00136266.
XX
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
XX
PI Nakagawara A;
XX
DR WPI; 2001-226686/23.
XX
PT Human 1p36 homozygosity deletion domain from the 36-position of first
PT chromosome short arm in human neuroblastoma cell lines, applicable e.g.
PT in gene diagnosis of tumors as well as in developing anti-cancer drugs.
XX
PS Example 8; Page 93-95; 226pp; Japanese.
XX
CC The present invention describes a homozygosity deletion domain co-
CC existing in the 36-position of the first chromosome short arm (1p36) in
CC human neuroblastoma. Also described are base sequences from the 1p36
CC position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1),
CC which are tumour suppressor genes in human neuroblastoma. The genes are
CC tumour suppressor genes, base sequence data of which are applicable as
CC tumour markers and reagents in studying mechanism of tumour body
CC formation, and gene diagnosis of tumours as well as in developing anti-
CC cancer drugs. AAF97787 to AAF97829 represent PCR primers used in the
CC exemplification of the present invention, and AAF97830 to AAF97874
CC represent sequences given in the exemplification of the present invention
XX
SQ Sequence 6405 BP; 1650 A; 1449 C; 1383 G; 1923 T; 0 U; 0 Other;

Query Match 16.7%; Score 416.2; DB 5; Length 6405;
Best Local Similarity 59.9%; Pred. No. 7e-76;
Matches 856; Conservative 1; Mismatches 504; Indels 68; Gaps 7;

```
Qy        603 GTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAG 662
Db       3636 GTCTTTATTTTTTATTTTTTTGAGGTGAGTTTCACTCTTGTTGCCCAGGCTGGAGTGCAA 3577

Qy        663 TGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC 722
Db       3576 TGGCACGATCTCAGCTTACAACAACCTCTGCCTCCTGAGTTCAAGTGATTCTCCTGCCTC 3517

Qy        723 AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAAT 782
Db       3516 AGCCTCCCGAGTAGCTGGGATTACAGGCATGCACCACCACACTCAGCTGATTTTTTGTA 3457

Qy        783 TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCA 842
Db       3456 TTTTTAGTAGAGA-TGGGGTTCTCCATGTTGGTCAGGCTAGTCTCAAACTCCCGACCTCA 3398

Qy        843 AGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTG 902
Db       3397 GGTGATCCGCCTGCCTCGGCCTCCCGAAGTGCTGGGATTACAGGCGTGAGCCATAAGGCC 3338

Qy        903 CGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGG 962
Db       3337 TGGCCTATTTTTTACT---------------------------------------------- 3322

Qy        963 ATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACC 1022
Db       3321 -TTTAAGATGGAGTTTTGCTCTTGTTGCCCAAGCTGGAGTGCAATGGCATGATC------ 3269

Qy       1023 TCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCT 1082
Db       3268 -----TCGGCTCACTGCAACCTCCGCCTCCCAGGTTCAAGTGATTCTCTTGCCTCAGTCT 3214

Qy       1083 CCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTTTA 1142
Db       3213 CCCAAGTAGCTGGGATTACAGGCATGCACCACCATGCCCGGCTAA--ATTTGTATTTTTA 3156

Qy       1143 GCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGAT 1202
Db       3155 GTAGAGATGGGGTTTCTCCATGTTGGTTAGGCTGGTCTCAAACTCCCAACCTC-AGTGAT 3097

Qy       1203 CTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCG 1262
Db       3096 GCACCAGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGGCCG 3037
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Qy       1263 ATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAG 1322
Db       3036 TACGTATCTTTATATCAGGATGTTTATAACAATTTTCTCTTAGAACATCTTTAGAATTTA 2977

Qy       1323 TAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCTTTT 1382
Db       2976 ATACTAGGAAAAAAGGTTT-------CTCTCGACAAACTATTAGGCTTTCTTTTACCAGA 2924

Qy       1383 TTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCACT 1442
Db       2923 GTGAAAATTGTACAATTTATCTTTCCCTTTTTGCATTAAATTCCATGTTCCAAATTAAAT 2864

Qy       1443 TATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTTCAT 1502
Db       2863 TACAATAACCACATTAGCCGAGGCAACCTATACATTTAGTTTTTCTTGTTACATAAATTT 2804

Qy       1503 TGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCA 1562
Db       2803 TTACTTATTTATATTTTAATAGCTTCACTGTATATATTTGTGGTAAGCTGCTCAAATCCT 2744

Qy       1563 CTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGAGAAATA 1622
Db       2743 TTCTAGAAGTAGTAACTGGTATAAATTATAAATAAATAAAAACTTCCTGTAATAGCCTAT 2684

Qy       1623 CACACACACACACACACTC-ACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAA 1681
Db       2683 TCTGCTATTTAACACTGTAAATATGTTGTGTAGTCAAAGTTCTAGTTCCTAAAAACAAAT 2624

Qy       1682 ACCTGCATTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGAC 1741
Db       2623 AAAACCAAACGACACAGCAAGCTTTTAAAAGTTACATAAAGATCGGCTGGGCATCGTGGC 2564

Qy       1742 TCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAA 1801
Db       2563 TCACGCGTATAATCCCAACACTTTGGGAGGCCAAGGCGGGTGGATCACTTGAGGTCAGGA 2504

Qy       1802 GTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAAAATTA 1861
Db       2503 GTTCAAGACCAGCCTGGCCAACATGATGAAACGCTGTCTCTACTAAAAATACAAAAATTA 2444

Qy       1862 GCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAT 1921
Db       2443 GCTGGGTGTGATGGCACATGACTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAAT 2384

Qy       1922 TGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCC 1981
Db       2383 CACTTGAACCCGGGAGATGAAGGTTGCAGTGAGCCAAGGTCACACCACTGCACTCTAGCC 2324

Qy       1982 TGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATAA 2030
Db       2323 TGGATGACAGAGCGAGACTCTGTCTCAAAAAAAAAAAAAGTTGCACAAA 2275
```

```
RESULT 11
ADP13332/c
ID   ADP13332 standard; DNA; 126990 BP.
XX
AC   ADP13332;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Renal cell carcinoma differentially expressed gene #68.
XX
KW   ds; diagnosis; non-blood disease; solid tumor; gene expression;
KW   peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW   head/neck cancer; differential expression.
XX
OS   Homo sapiens.
XX
PN   WO2004048933-A2.
XX
PD   10-JUN-2004.
XX
PF   21-NOV-2003; 2003WO-US037481.
XX
PR   21-NOV-2002; 2002US-0427982P.
PR   03-APR-2003; 2003US-0459782P.
XX
PA   (AMHP ) WYETH.
PA   (TWIN/) TWINE N C.
PA   (BURC/) BURCZYNSKI M E.
PA   (TREP/) TREPICCHIO W L.
PA   (DORN/) DORNER A.
PA   (STOV/) STOVER J A.
PA   (SLON/) SLONI D K.
XX
PI   Twine NC,  Burczynski ME,  Trepicchio WL,  Dorner A,  Stover JA;
PI   Sloni DK;
XX
DR   WPI; 2004-460799/43.
XX
PT   Diagnosing non-blood disease such as solid tumor, involves comparing
PT   differential expression profile of specific genes in peripheral blood
PT   sample of subject with reference expression profile of specific genes.
XX
PS   Disclosure; SEQ ID NO 68; 350pp; English.
XX
CC   The invention relate to a method of diagnosing (M1) non-blood disease
CC   such as solid tumor by providing peripheral blood sample of human having
CC   non-blood disease, and comparing an expression profile of specific genes
CC   in the peripheral blood sample to reference expression profile of the
CC   genes, where each of the genes is differentially expressed in peripheral
CC   blood mononuclear cells (PBMCs) of patients having the disease as
CC   compared to PBMCs of normal humans. The method is useful for diagnosing
CC   non-blood disease such as solid tumor. The solid tumor is chosen from
CC   renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC   peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC   sample is a whole blood sample (claimed). (M1) is useful for identifying
CC   genes that are differentially expressed in peripheral blood samples
CC   isolated at different stages of progression, development or treatment of
CC   RCC and/or other solid tumors. This sequence corresponds to a gene that
CC   is differentially expressed and detected by the method of the invention.
CC   (Note: this sequence is not given as part of the printed specification
CC   but was obtained from WIPO in electronic format at
CC   ftp.wipo./pub/published_pct_sequences).
XX
SQ   Sequence 126990 BP; 36683 A; 27389 C; 27065 G; 35853 T; 0 U; 0 Other;
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  Query Match             16.6%;  Score 416;  DB 12;  Length 126990;
  Best Local Similarity   60.2%;  Pred. No. 1.4e-75;
  Matches  859;  Conservative    1;  Mismatches  536;  Indels   32;  Gaps    9;

Qy        611 TTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTGGTGCAA 670
Db      27332 TTTCTCTAATGCTGAGATGGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGTGA 27273

Qy        671 CCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCC 730
Db      27272 TCTCA-----------CCTCCACCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCT-CC 27225

Qy        731 AAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATTTTTTTGT 790
Db      27224 TGGTAGCTGGGAATACAGGCGTGCACCACCATGCCCGGCTAATTTTTATA--TTTTCAGT 27167

Qy        791 AGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCC 850
Db      27166 AGAGTCGCAGTTTCACCATGTTTCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCC 27107

Qy        851 TCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACT 910
Db      27106 ACCCGCCGCAGCCTCCCAACGTGCTGGGATAATAGGGGTGAGCCACTGCACCTGGCCTTT 27047

Qy        911 TATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTGC 970
Db      27046 CTGTACTCTTTATTCTATTTCACTGGTCTGTTTCTTTTGGTTTCAGTATCATAGTACTTT 26987
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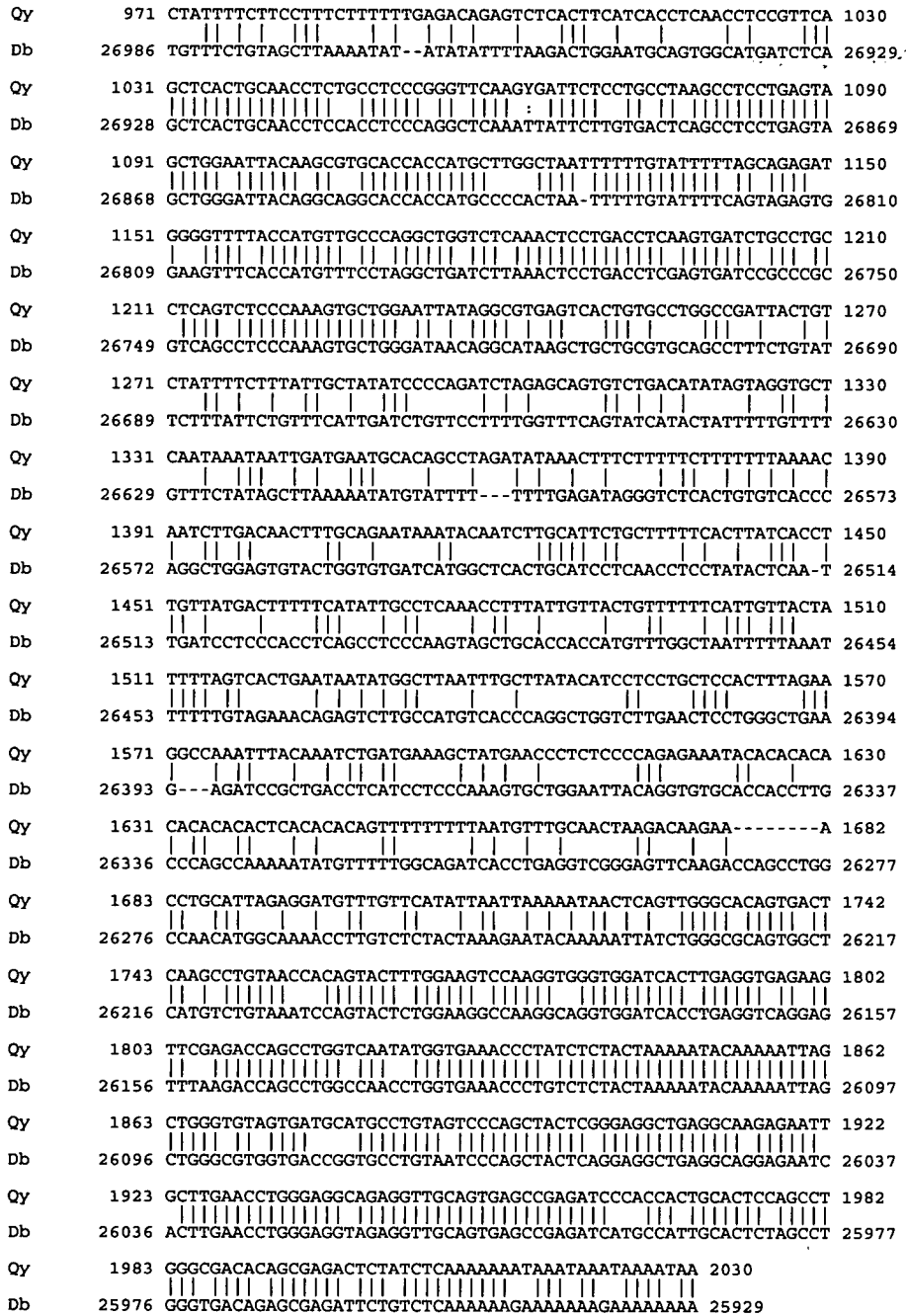
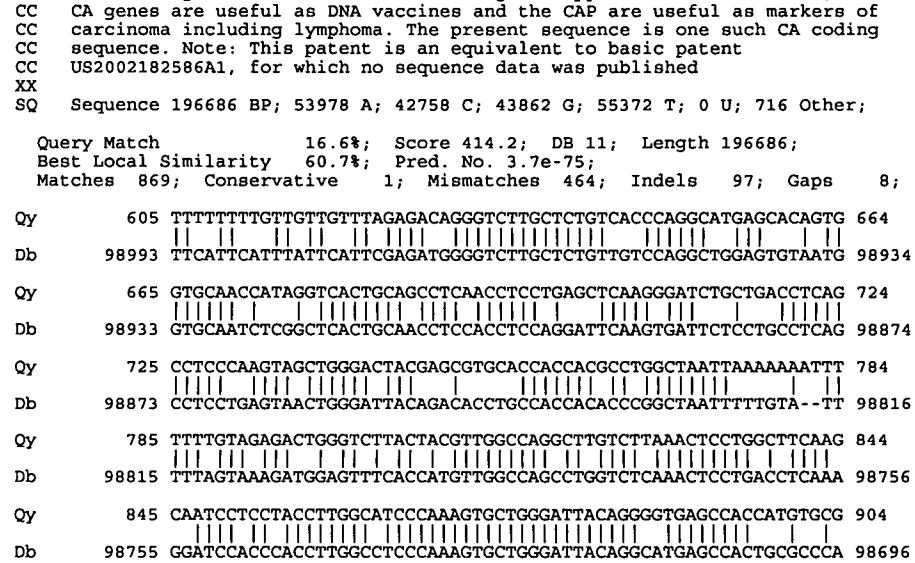


RESULT 12
ACN44170/c
ID ACN44170 standard; DNA; 196686 BP.
XX
AC ACN44170;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genomic sequence hCG39530.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 484; 0pp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 196686 BP; 53978 A; 42758 C; 43862 G; 55372 T; 0 U; 716 Other;

Query Match 16.6%; Score 414.2; DB 11; Length 196686;
Best Local Similarity 60.7%; Pred. No. 3.7e-75;
Matches 869; Conservative 1; Mismatches 464; Indels 97; Gaps 8;



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Qy       905 GCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGAT 964
             || |  ||  | | ||  |   | | ||   |    |       |||      |   |
Db     98695 GCCATGTACATTTATAATTGTACTATATCTCCTTTGGT--------CACCATCTTGTCTT 98644

Qy       965 TACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCTC 1024
             |  |   | |||| ||  ||| ||||||||||||||||||  ||   || ||    |
Db     98643 TTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTTGCTCTGTCGCCCAGGCTGG 98584

Qy      1025 CGT--------------TCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTC 1070
              ||              || |||||||||| ||| ||||||| || ||| |: ||||||
Db     98583 AGTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTCCGCCTCCCTGGCTCACGCCATTCTC 98524

Qy      1071 CTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTT 1130
             |||||| ||||||| |||||||||| | |||| | |  |||||||| ||  ||  |||||
Db     98523 CTGCCTCAGCCTCCAGAGTAGCTGGGACTACATGTGCCCACCACCACGCCCGGAGAATTT 98464

Qy      1131 TTTGTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTG 1190
             |||||||||||    |||| ||||||| ||| ||||  ||||| ||||||| | ||||||
Db     98463 TTTGTATTTTTAATGGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTG 98404

Qy      1191 ACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCAC 1250
             |||||  ||||||  ||  |||||| |||||||||||||| |||| ||| ||||| |||
Db     98403 ACCTC--GTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGTGAGCCAC 98346

Qy      1251 TGTGCCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTG 1310
             || ||| ||||     ||     | |  ||  ||  | | | | |   | ||||
Db     98345 TGGGCCCGGCCACCACCTCGTCTTCTGATTGCTTTTTTTTTTCACTTCTGGAGAG----- 98291

Qy      1311 TCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTT 1370
                                                                |  || |
Db     98290 ----------------------------------------------------AGGAAATC 98283

Qy      1371 TCTTTTTCTTTTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTC 1430
             | | | |  ||    | | |  |  |  |  |||| |     |   ||  ||||   | |
Db     98282 TATATGTTCTTCACCATATCTCTAATACCTTCTTTACCTTCTCTCTAATATCTAATACTA 98223

Qy      1431 TGCTTTTTCACTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTATTGTTA 1490
             |   |   || |||    |   |||   | |        |   |   |   |   | |
Db     98222 TATATACATACATATAGTGTGTATATATATATGCATGTATATATAGTATTATATGTATAT 98163

Qy      1491 CTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACAT 1550
              | |  |  |   |||  |||||  || |   | |  |     | |   || || | ||
Db     98162 ATATAATAACCAGGTTCTTATTTATGTTATCCATTGCTTGAATTAACAATGTTTTTTCA- 98104

Qy      1551 CCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTC 1610
                   |  | | ||| ||  |   |       ||||| ||  |       |  |
Db     98103 -------AAACCTATAAAAAGACCTTAAACAAGGTAAGGATGAGAGGAACCTTGAGTTGC 98051

Qy      1611 CCCAGAGAAATACACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAAC 1670
             || ||| |||           |                  | | |||||| | |  |
Db     98050 CCAAGATAAAATTTTGTCTCAAAGTCTCTCACTTTGTTTCATGTGTTTAATCTCTCAATA 97991

Qy      1671 TAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAAAAATAA----CTCA 1726
             ||    |   |      |||| |  |  |||  |  |  | |  ||||||||    ||
Db     97990 TATTTAATCTATTGGCAATTACAATAATTTTTGTTTTGGTCACAAAAAATAAGCTCCTGG 97931

Qy      1727 GTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGAT 1786
             | ||| ||| |||| |||| |||||||| | ||| |||||| || || ||| ||||||||
Db     97930 GCTGGACACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGAGGGTGGAT 97871

Qy      1787 CACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTA 1846
             |||   |||| || || | ||||||| ||||| ||| ||||| |||| || |||||||||
Db     97870 CAC--CAGGTCAGGAGATGGAGACCATCCTGGCCAACATGGTAAAACTCTGTCTCTACTA 97813

Qy      1847 AAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGG 1906
             |||||||||||||||||||| || |||      ||||||||||||||||||||||||||
Db     97812 CAAATACAAAAATTAGCTGGGCGTGGTGGCATGCGCCTGTAGTCCCAGCTACTCGGGAGG 97753

Qy      1907 CTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCAC 1966
             |||||||| ||||| |||||||||||||||||||| ||||||| |||| |||||| | |
Db     97752 CTGAGGCAGGAGAACTGCTTGAACCTGGGAGGCAGACGTTGCAGCGAGCTGAGATCACGC 97693
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Qy      1967 CACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAA 2017
             |||||||||||||||||||| |||| ||||||||||||||||||||||  ||
Db     97692 CACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCTATCTCAAAAAATAAA 97642
```

RESULT 13
ADP68568/c
ID ADP68568 standard; cDNA; 86000 BP.
XX
AC ADP68568;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human PPAR-alpha cDNA.
XX
KW cytostatic; gene therapy; PPAR-alpha;
KW peroxisome proliferator-activated receptor-alpha; PPAR-alpha modulator;
KW PPAR-alpha associated disorder; hyperproliferative disorder; human; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN US2004115637-A1.
XX
PD 17-JUN-2004.
XX
PF 11-DEC-2002; 2002US-00317500.
XX
PR 11-DEC-2002; 2002US-00317500.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Mckay R, Dobie KW;
XX
DR WPI; 2004-449378/42.
XX
PT New oligonucleotide compound that inhibits expression of PPAR-alpha,
PT useful for preparing a composition for treating hyperproliferative
PT disorders, e.g. cancer.
XX
PS Claim 1; SEQ ID NO 4; 121pp; English.
XX
CC The invention describes a compound, having a sequence comprising 8-80 bp
CC targeted to a nucleic acid encoding PPAR-alpha (peroxisome proliferator-
CC activated receptor-alpha), that specifically hybridises with the nucleic
CC acid encoding PPAR-alpha comprising 86001-bp sequence and inhibits
CC expression of PPAR-alpha. Also described are: a method of inhibiting the
CC expression of PPAR-alpha in cells or tissues; a method of screening for a
CC modulator of PPAR-alpha; a diagnostic method for identifying a disease
CC state; a kit or assay device comprising the compound; and a method of
CC treating an animal having a disease or condition associated with PPAR-
CC alpha. The oligonucleotide compound is useful for preparing a composition
CC for treating hyperproliferative disorder e.g. cancer. This sequence
CC represents a human peroxisome proliferator-activated receptor-alpha (PPAR
CC -alpha) cDNA.
XX
SQ Sequence 86000 BP; 22822 A; 19623 C; 20377 G; 23178 T; 0 U; 0 Other;

  Query Match   16.6%; Score 413.6; DB 12; Length 86000;
  Best Local Similarity 61.0%; Pred. No. 4.1e-75;
  Matches 878; Conservative   1; Mismatches 490; Indels   71; Gaps   10;

```
Qy        605 TTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTG 664
              ||||||||  | || ||| ||||| | |||   ||||||| |||||||  |||  |||||
Db      69228 TTTTTTTTTCTTTTTTTTTGAGACGGAGTCGCACTCTGTCGCCCAGGCTGGAGTGCAGTG 69169

Qy        665 GTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAG 724
              |||| | |  || |||||||| |||| ||||| | | |||||  ||   |   ||||
Db      69168 GTGCGATCTCAGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCTATTCTCCTGTCTCAT 69109

Qy        725 CCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATTT 784
              |||||||||||||||||| |||  | |||||| |||| |||  |||||||     |  ||
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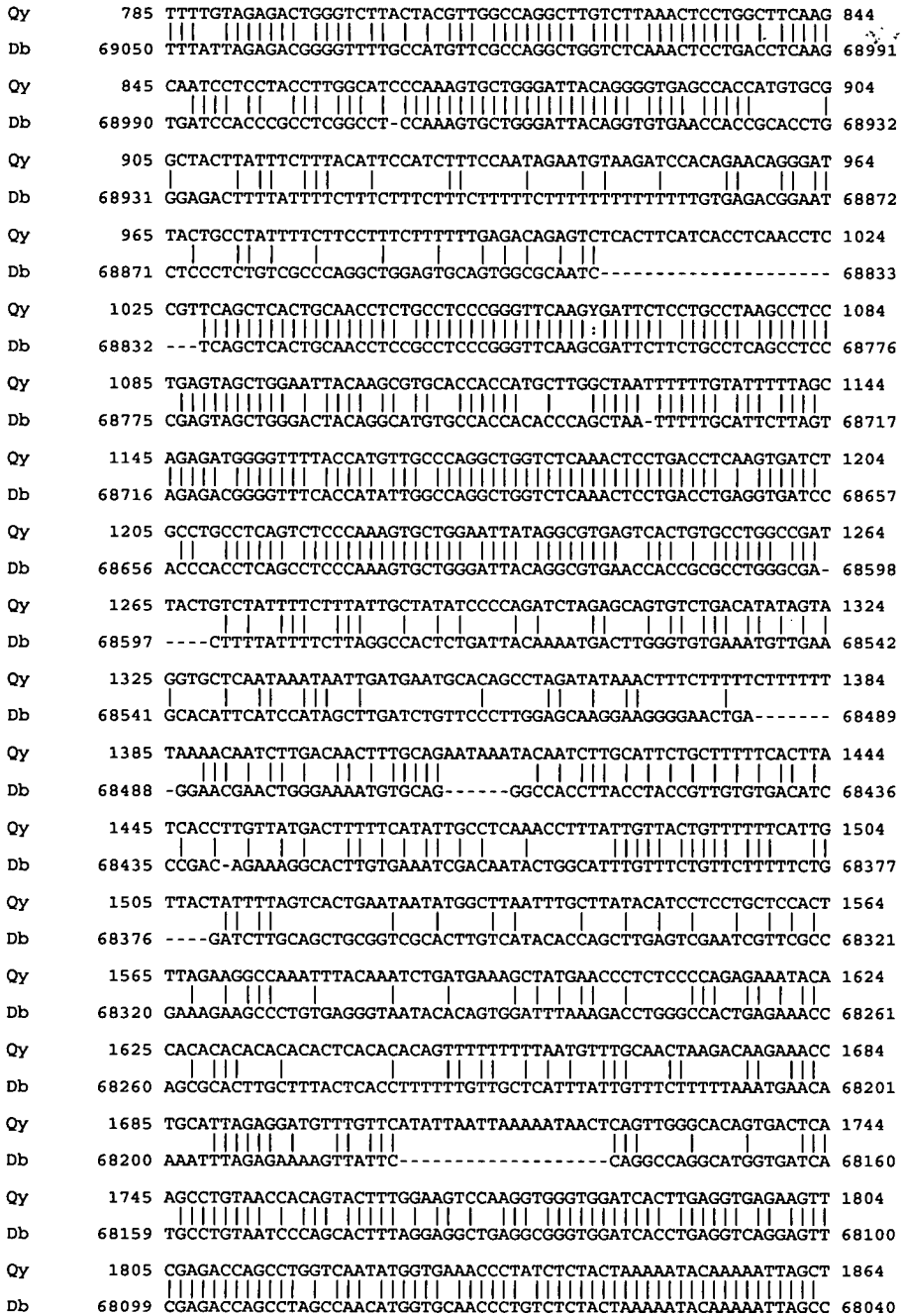
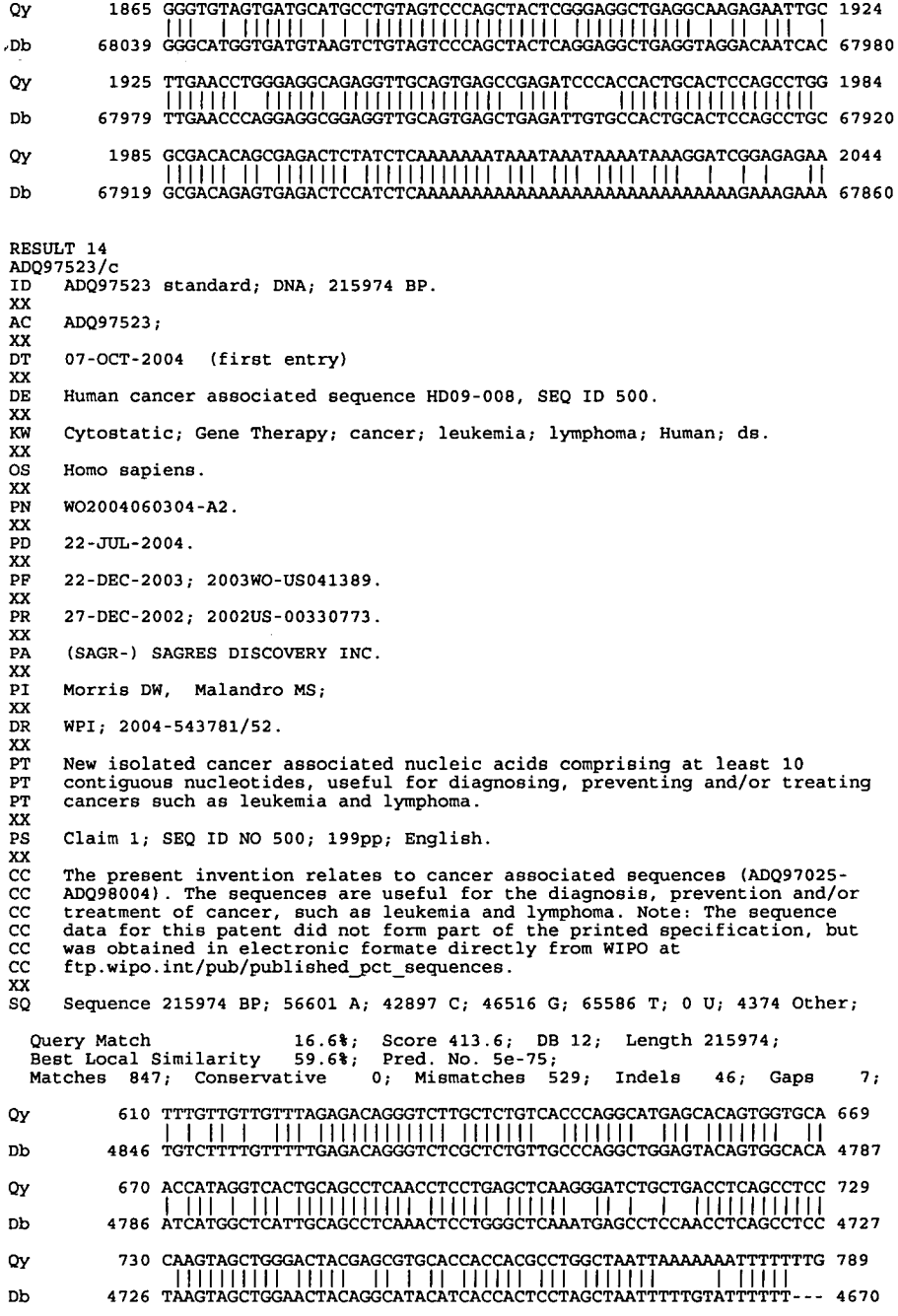
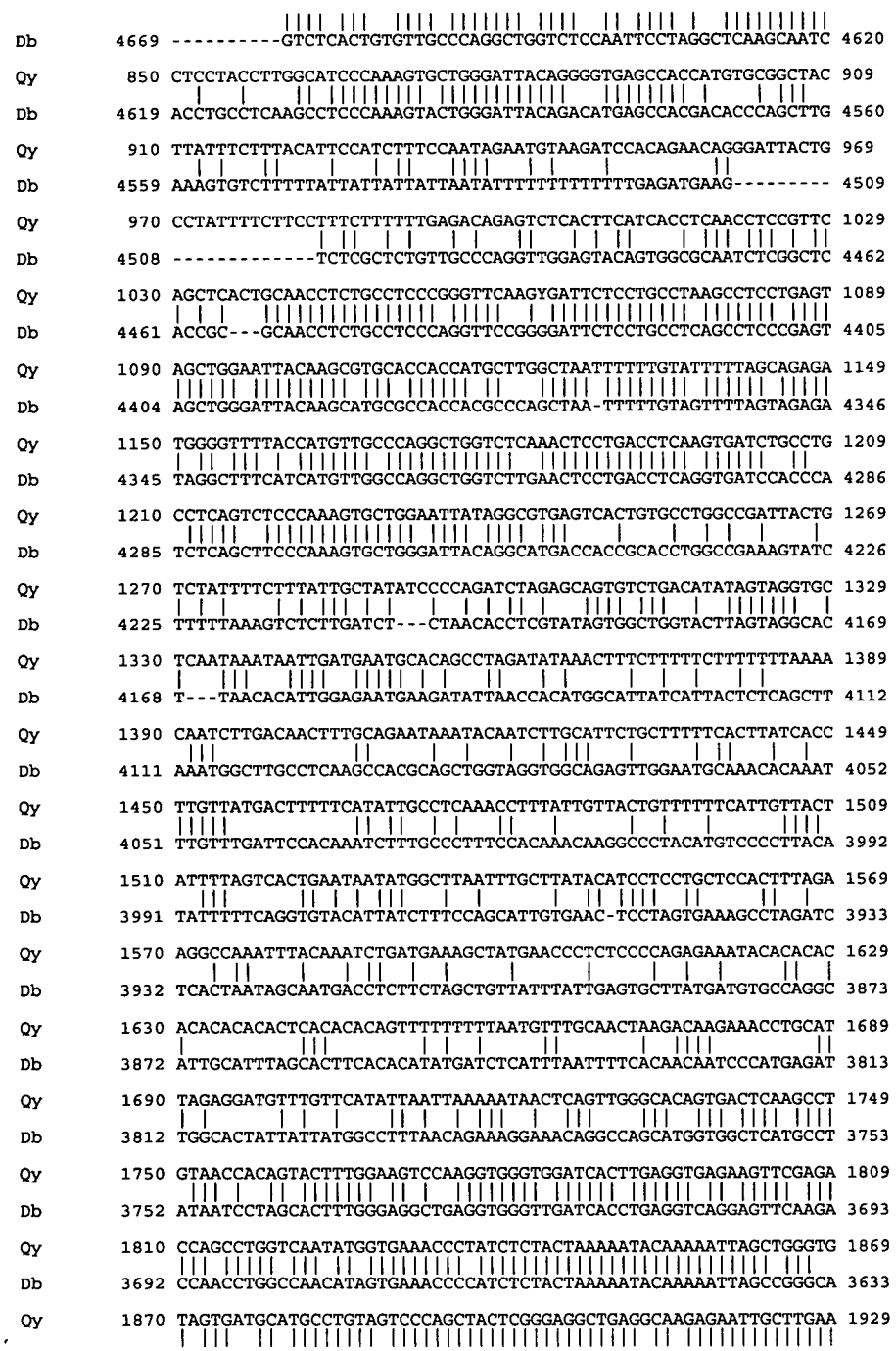
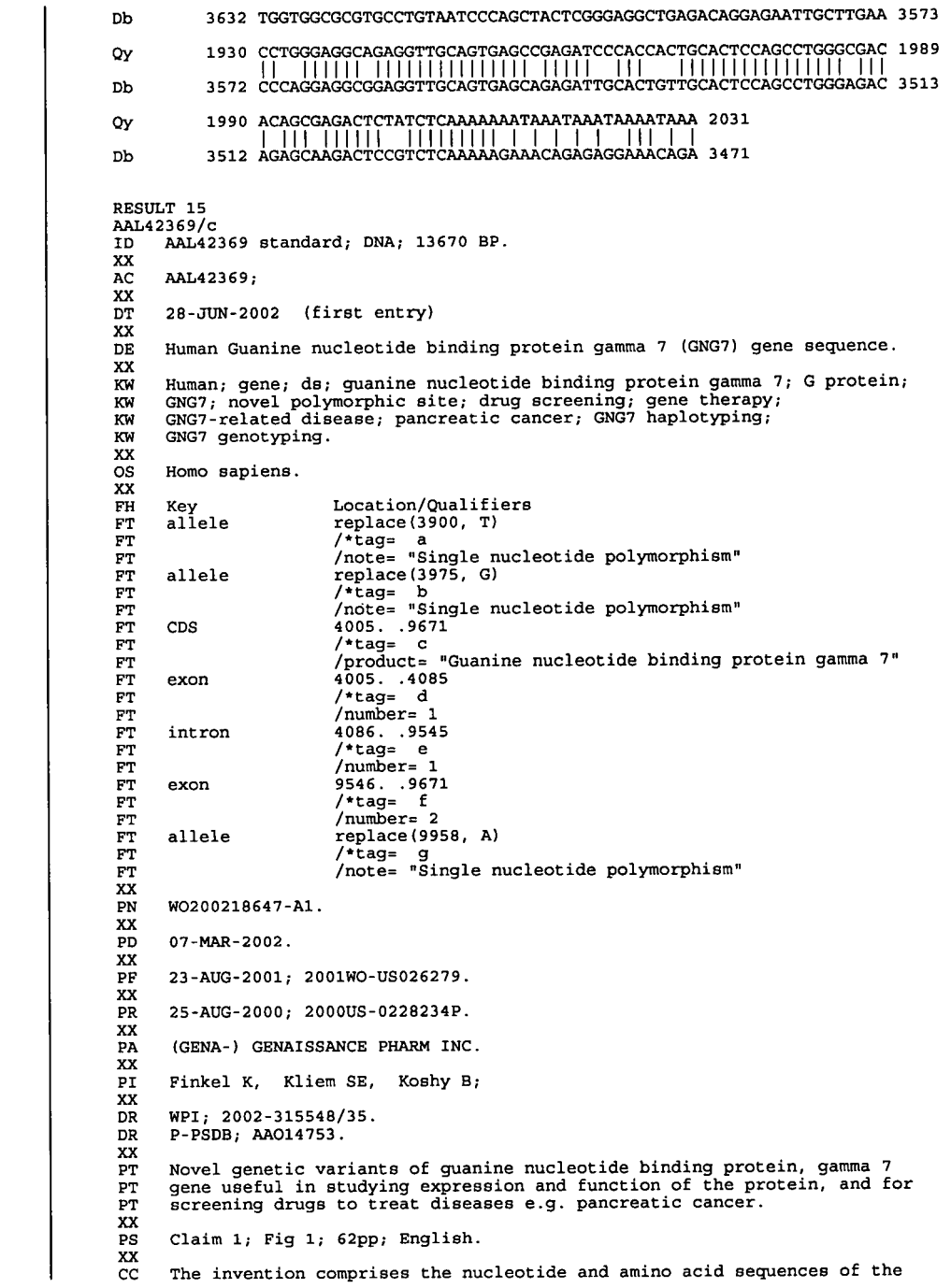




RESULT 14
ADQ97523/c
ID ADQ97523 standard; DNA; 215974 BP.
XX
AC ADQ97523;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cancer associated sequence HD09-008, SEQ ID 500.
XX
KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds.
XX
OS Homo sapiens.
XX
PN WO2004060304-A2.
XX
PD 22-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US041389.
XX
PR 27-DEC-2002; 2002US-00330773.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-543781/52.
XX
PT New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.
XX
PS Claim 1; SEQ ID NO 500; 199pp; English.
XX
CC The present invention relates to cancer associated sequences (ADQ97025-
CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic formate directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 215974 BP; 56601 A; 42897 C; 46516 G; 65586 T; 0 U; 4374 Other;

Query Match 16.6%; Score 413.6; DB 12; Length 215974;
Best Local Similarity 59.6%; Pred. No. 5e-75;
Matches 847; Conservative 0; Mismatches 529; Indels 46; Gaps 7;





RESULT 15
AAL42369/c
ID AAL42369 standard; DNA; 13670 BP.
XX
AC AAL42369;
XX
DT 28-JUN-2002 (first entry)
XX
DE Human Guanine nucleotide binding protein gamma 7 (GNG7) gene sequence.
XX
KW Human; gene; ds; guanine nucleotide binding protein gamma 7; G protein;
KW GNG7; novel polymorphic site; drug screening; gene therapy;
KW GNG7-related disease; pancreatic cancer; GNG7 haplotyping;
KW GNG7 genotyping.
XX
OS Homo sapiens.
XX

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PN WO200218647-A1.
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PD 07-MAR-2002.
XX
PF 23-AUG-2001; 2001WO-US026279.
XX
PR 25-AUG-2000; 2000US-0228234P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Finkel K, Kliem SE, Koshy B;
XX
DR WPI; 2002-315548/35.
DR P-PSDB; AAO14753.
XX
PT Novel genetic variants of guanine nucleotide binding protein, gamma 7
PT gene useful in studying expression and function of the protein, and for
PT screening drugs to treat diseases e.g. pancreatic cancer.
XX
PS Claim 1; Fig 1; 62pp; English.
XX
CC The invention comprises the nucleotide and amino acid sequences of the

```
CC   human guanine nucleotide binding protein (G protein) gamma 7 (GNG7). The
CC   invention specifically relates to the discovery of three novel
CC   polymorphic sites in the GNG7 gene. The GNG7 nucleotide and protein
CC   sequences are useful for screening for drugs which target GNG7 and may be
CC   used to treat (gene therapy) GNG7-related diseases (e.g. pancreatic
CC   cancer). The GNG7 nucleotide sequence can be used for haplotyping GNG7,
CC   genotyping GNG7 and predicting the haplotype pair for GNG7 in an
CC   individual. The present DNA sequence represents the human GNG7 gene
CC   sequence
XX
SQ   Sequence 13670 BP; 3047 A; 3946 C; 3680 G; 2997 T; 0 U; 0 Other;

  Query Match            16.5%;  Score 413.4;  DB 6;  Length 13670;
  Best Local Similarity  60.6%;  Pred. No. 3.1e-75;
  Matches  876;  Conservative    1;  Mismatches  512;  Indels   56;  Gaps   10;

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Qy       1964 CACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAAT 2023
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Qy       2024 AAAAT 2028
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Job time : 1487 secs
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 09:56:20 ; Search time 12639 Seconds
(without alignments)
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Perfect score: 2499
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_in:*
3: gb_env:*
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14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	9	460.4	18.4	150266	8	AC022408	AC022408 Homo sapi
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c	22	439.4	17.6	180076	14	AC022177	AC022177 Homo sapi
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ALIGNMENTS

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DEFINITION Homo sapiens phospholipase A2, group IB (pancreas) (PLA2G1B) gene, complete cds.
ACCESSION AY438977
VERSION AY438977.1 GI:37953284
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 8368)
AUTHORS Rieder,M.J., Livingston,R.J., Daniels,M.R., Chung,M.-W., Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D., Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2003) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).
FEATURES Location/Qualifiers
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Qy        841 CAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATG 900
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Db       4214 CAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATG 4273

Qy        901 TGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAG 960
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Qy        961 GGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAA 1020
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Qy       1021 CCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGC 1080
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Db       4394 CCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTAAGC 4453

Qy       1081 CTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTT 1140
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Qy       1141 TAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4514 TAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG 4573

Qy       1201 ATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGC 1260
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Db       4574 ATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGC 4633

Qy       1261 CGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATAT 1320
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Qy       1381 TTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCA 1440
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Qy       1441 CTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTTC 1500
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Qy       1501 ATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTC 1560
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Qy       1561 CACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGAGAAA 1620
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Qy       1621 TACACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGA 1680
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Qy       1681 AACCTGCATTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGA 1740
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Qy       1801 AGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAAAATT 1860
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Qy       1861 AGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAA 1920
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Db       5234 AGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAA 5293

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Qy       1981 CTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATAAAGGATCGGAG 2040
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Qy       2041 AGAAACAAAACTAATAAGATTCCTGAAGGTAAGCAGAGATACGTAAATTATATGTAATAA 2100
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Db       5474 AGTTTAAATGCATTTTAACTGTAATCTTATTGTTTATTTTGGTTATAAAAGTAAACAAGC 5533

Qy       2161 CAAAAGTAATGCAACTTCAAACKCTACATAAATATCTATTATGGAAAGTGGAAGGCATCT 2220
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Db       5534 CAAAAGTAATGCAACTTCAAACTCTACATAAATATCTATTATGGAAAGTGGAAGGCATCT 5593

Qy       2221 ATAATCCTACTACCCAAAGATAACCAGTTACATATTCCTCCAGATTTTTGGGGCATACAC 2280
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Qy       2281 TAGCTTTTTTTATTTGGGAAAATTTCCATGTGCAGGCATACCTAATTTTTCTAAATGTCT 2340
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Qy       2341 ATGTAGTATTCCATTTAAGGATGTTCCATAATTTTTAAAATACATGCTTTAAAGTAGAGA 2400
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Db       5714 ATGTAGTATTCCATTTAAGGATGTTCCATAATTTTTAAAATACATGCTTTAAAGTAGAGA 5773

Qy       2401 AACTAGGTTGGGCATGGTGGCTCACGCCTGTATCCCAGCACTTTGGGAGGCCGAGGCAAA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5774 AACTAGGTTGGGCATGGTGGCTCACGCCTGTATCCCAGCACTTTGGGAGGCCGAGGCAAA 5833

Qy       2461 TGGATCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGACAA 2501
             |||||||||||||||||||||||||||||||||||||||||
Db       5834 TGGATCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGACAA 5874


RESULT 2
AX377239
LOCUS       AX377239               13612 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 1 from Patent WO0212562.
ACCESSION   AX377239
VERSION     AX377239.1  GI:19573528
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kazemi,A., Kliem,S.E. and Koshy,B.
  TITLE     Haplotypes of the pla2g1b gene
  JOURNAL   Patent: WO 0212562-A 1 14-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /note="PS1: polymorphic base G or A"
     variation       3968
                     /note="PS2: polymorphic base A or G"
     variation       6060
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     variation       6844
                     /note="PS4: polymorphic base G or A"
     variation       9531
                     /note="PS5: polymorphic base G or A"
ORIGIN

  Query Match             99.9%;  Score 2497.4;  DB 6;  Length 13612;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2496;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCGTGTCACTGCTGTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6516 GTCGTGTCACTGCTGTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATG 6575

Qy         61 CTTTCAATAAATATATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCC 120
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Db       6576 CTTTCAATAAATATATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCC 6635

Qy        121 TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGGCTGAC 180
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Db       6636 TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGGCTGAC 6695

Qy        181 CTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGA 240
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Db       6696 CTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGA 6755

Qy        241 CACATGACAACTGCTACGACCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACA 300
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Db       6756 CACATGACAACTGCTATGACCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACA 6815

Qy        301 MMCCGTACACCCACACCTATTCATACTCRTGCTCTGGCTCGGCAATCACCTGTAGCAGTA 360
              ::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6816 ACCCGTACACCCACACCTATTCATACTCRTGCTCTGGCTCGGCAATCACCTGTAGCAGTA 6875

Qy        361 GGTTTATCCCTTCCTTGACCTATGAATTCTAGTTGGTTCTCAGTAGGCCGGGGGGAAATA 420
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Qy        421 ATAGTAACAACAGCCATGATTTAGTGTTAATTTTCTTGGTTCTGGGCAGTGTCTCCTTTA 480
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Db       6936 ATAGTAACAACAGCCATGATTTAGTGTTAATTTTCTTGGTTCTGGGCAGTGTCTCCTTTA 6995

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Db       6996 ATCCTCAGAACAACACTATGGGATAGGTACAATTATCCTCACTTAACAGATAAGAAAACT 7055

Qy        541 GAGGCTCAGAAGGCTGAGCTATTTGCCCAAGATCACACAGCTTGTAAGTGGTGACAGTTT 600
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Db       7056 GAGGCTCAGAAGGCTGAGCTATTTGCCCAAGATCACACAGCTTGTAAGTGGTGACAGTTT 7115

Qy        601 GGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCAC 660
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Db       7116 GGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCAC 7175

Qy        661 AGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACC 720
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Db       7176 AGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACC 7235

Qy        721 TCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAA 780
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Db       7236 TCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAA 7295

Qy        781 ATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTT 840
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Db       7296 ATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTT 7355

Qy        841 CAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATG 900
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Db       7356 CAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATG 7415

Qy        901 TGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAG 960
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Db       7416 TGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAG 7475

Qy        961 GGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAA 1020
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Db      7476 GGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAA 7535
Qy      1021 CCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGC 1080
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Qy      1081 CTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTT 1140
Db      7596 CTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTT 7655
Qy      1141 TAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG 1200
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Qy      1321 AGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCTT 1380
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Qy      1381 TTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCA 1440
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Qy      1441 CTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTTC 1500
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Qy      1681 AACCTGCATTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGA 1740
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Qy      1861 AGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAA 1920
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Qy      2281 TAGCTTTTTTTATTTGGGAAAATTTCCATGTGCAGGCATACCTAATTTTTCTAAATGTCT 2340
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Qy      2341 ATGTAGTATTCCATTTAAGGATGTTCCATAATTTTTAAAATACATGCTTTAAAGTAGAGA 2400
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RESULT 3
AC003982/c
LOCUS       AC003982              122302 bp    DNA     linear   PRI 18-MAR-1999
DEFINITION  Homo sapiens PAC clone 166H1 from 12q, complete sequence.
ACCESSION   AC003982
VERSION     AC003982.1  GI:2769695
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Hominidae; Homo.
REFERENCE   1  (bases 1 to 122302)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
   PUBMED   9847074
REFERENCE   2  (bases 1 to 122302)
  AUTHORS   Bradshaw,H., Wu,X. and Ozersky,P.
  TITLE     The sequence of Homo sapiens PAC clone 166H1
  JOURNAL   Unpublished (1999)
REFERENCE   3  (bases 1 to 122302)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1998) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   4  (bases 1 to 122302)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-1999) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     SUBMITTED BY:  WUGSC
            Genome Sequencing Center
            Department of Genetics
            Washington University
            St. Louis MO 63108, USA
            http://genome.wustl.edu/gsc
            mailto:sapiens@watson.wustl.edu

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
```

between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
This clone was originally isolated in the laboratory of Professor Graeme Bell, Howard Hughes Medical Institute and Departments of Biochemistry and Molecular Biology, and Medicine, The University of Chicago, Chicago, IL, USA. The clone was provided by the laboratory of Dr. Roger Cox at The Wellcome Trust Centre For Human Genetics, Oxford, UK. Some contig information was also obtained from Yamagata et al., Nature 384:455-8 (1996).

SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-1, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.
The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is 278C19; the clone sequenced to the right is 15E1. Actual start of this clone is at base position 1 of 166H1; actual end is at 122302 of 166H1.

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FEATURES             Location/Qualifiers
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                     /clone="166H1"
                     /clone_lib="RPCI-1"
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RESULT 4
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LOCUS       AC078926               220384 bp    DNA     linear   HTG 26-MAR-2002
DEFINITION  Homo sapiens chromosome 12 clone RP11-836M11, WORKING DRAFT
            SEQUENCE, 11 unordered pieces.
ACCESSION   AC078926
VERSION     AC078926.23  GI:19718703
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 220384)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 220384)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-AUG-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 220384)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Mar 26, 2002 this sequence version replaced gi:18449664.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: HCAM
                Center clone name: RP11-836M11
            -------------- Summary Statistics
                Sequencing vector: Plasmid;
                Sequencing vector: M13;
                Chemistry: Dye-primer Bodipy: 47% of reads
                Chemistry: Dye-terminator Big Dye: 53% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 234783 bases at least Q40
                Consensus quality: 241821 bases at least Q30
                Consensus quality: 245671 bases at least Q20
                Estimated insert size: 219187; sum-of-contigs estimation
                Quality coverage: 8.9x in Q20 bases; sum-of-contigs estimation
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            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 11 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2156: contig of 2156 bp in length
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ACCESSION   AC073930
VERSION     AC073930.23  GI:18958593
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 189729)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 189729)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 189729)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Feb 27, 2002 this sequence version replaced gi:14861669.
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                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
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                Assembly program: Phrap; version 0.990329
                Consensus quality: 191640 bases at least Q40
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                Quality coverage: 0x in Q20 bases; agarose-fp estimation
                Quality coverage: 11.7x in Q20 bases; sum-of-contigs estimation
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            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    64773: contig of 64773 bp in length
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ORIGIN

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Qy        510 CAATTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGGCTGAGCTATTTGCCCA 569
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Qy        570 AGATCACACAGCTTGTAAGTGGTGACAGTTTGGGTTTTTTTTTGTTGTTGTTTAGAGACA 629
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Qy        630 GGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCT 689
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Qy        930 TTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTT 989
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Qy        990 TTTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTCAGCTCACTGCAACCTCTGCC 1049
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LOCUS       AC068981              178887 bp    DNA     linear   HTG 01-SEP-2000
DEFINITION  Homo sapiens chromosome 15 clone RP11-580I7, WORKING DRAFT
            SEQUENCE, 37 unordered pieces.
ACCESSION   AC068981
VERSION     AC068981.3  GI:9958291
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 178887)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 178887)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Sep 1, 2000 this sequence version replaced gi:8748938.

            ---------------- Genome Center -----------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            -------------- Project Information --------------
            Center project name: H_NH0580I07
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 100%
            Sequencing vector: plasmid; 0%
            Chemistry: Dye-primer ET; 100% of reads
            Chemistry: Dye-terminator Big Dye; 0% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 157045 bases at least Q40
            Consensus quality: 163476 bases at least Q30
            Consensus quality: 167183 bases at least Q20
            Insert size: 192000; agarose-fp
            Insert size: 174828; sum-of-contigs
            Quality coverage: 3.01 in Q20 bases; agarose-fp
            Quality coverage: 3.40 in Q20 bases; sum-of-contigs
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 37 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *     4965     7695: contig of 2731 bp in length
            *     7696     7795: gap of unknown length
            *     7796    10187: contig of 2392 bp in length
            *    10188    10287: gap of unknown length
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            *    12304    12403: gap of unknown length
            *    12404    14390: contig of 1987 bp in length
            *    14391    14490: gap of unknown length
            *    14491    16285: contig of 1795 bp in length
            *    16286    16385: gap of unknown length
            *    16386    18364: contig of 1979 bp in length
            *    18365    18464: gap of unknown length
            *    18465    20794: contig of 2330 bp in length
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  Query Match             18.5%;  Score 462.6;  DB 14;  Length 178887;
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  Matches  890;  Conservative    1;  Mismatches  485;  Indels   57;  Gaps    8;

Qy        600 TGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCA 659
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Db      90620 TGTGTATTTTGTTGTTGTTGTTGTTGAGCCAGCTCGGGCTCTGTCGCCCAGGCTGGAGTG 90561

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Qy       1620 ATACACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAG 1679
Db      89652 CAATTTACAGACTTTCAAAAATTGATTTGGTTTCTACTGAAATAAAACGTAGAGGAAAAG 89593

Qy       1680 AAACCTGCA---TTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACA 1736
Db      89592 AACACAGTAAGCTAAAATGATGGAATTCAATCCCTTAAAAACAAAATTCAGCCGGGCACG 89533

Qy       1737 GTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGT 1796
Db      89532 TTGGCTCACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGTAGGTGGATCAC--GAGGT 89475

Qy       1797 GAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAA 1856
Db      89474 CAGGGGCTCGAGACCAGCCTGACCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAA 89415

Qy       1857 AATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAG 1916
Db      89414 AATTAGCTGGGTGTGGTGGCGGGCGCCTGTAATACCAGCTACTCAGGAGGCTGAGGCAGG 89355

Qy       1917 AGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTC 1976
Db      89354 AGAATTGCTTGAACCCGGGAGGCGGAAGCTGCAGTGAGCCGAGATCACGCCACTATACTC 89295
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Qy       1977 CAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATA 2029
Db      89294 CAGCCTGGGCGACAGAGCCAGACTCCGTCTCAAAAAACAAAAAAAAAAAAACA 89242
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RESULT 7
AC009244
LOCUS       AC009244               190162 bp    DNA     linear   PRI 26-MAY-2002
DEFINITION  Homo sapiens chromosome 7 clone RP11-305M3, complete sequence.
ACCESSION   AC009244
VERSION     AC009244.25  GI:21217399
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 190162)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
            and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 190162)
  AUTHORS   Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-AUG-1999) Human Genome Center, University of
            Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 190162)
  AUTHORS   Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
            Olson,M.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-OCT-2000) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   4  (bases 1 to 190162)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
            and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAY-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On May 26, 2002 this sequence version replaced gi:11038533.
            -------------- Genome Center
                Center: University of Washington Genome Center
                Center Code: UWGC
                Web site: http://www.genome.washington.edu
                Contact: uwgchtgs@u.washington.edu
            -------------- Project Information
                Center project name: chr-7
                Center clone name: RP11-305M3 (djs195)
            ------------- Summary Statistics
                Assembly program: Phrap; version 0.990319
                Consensus quality: 189969 bases at least Q40
                Consensus quality: 190110 bases at least Q30
                Consensus quality: 190161 bases at least Q20
                Insert size: 190162; sum-of-contigs
                Quality coverage: 9.7x in Q20 bases; sum-of-contigs
            --------------.
            Overlapping Sequences:
                5':  RP11-382M23 (UWGC:djs734g) AC093149 1340-bp overlap
                3':  RP11-448A19 (UWGC:djs705) AC078846 8765-bp overlap
            --------------------
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible from the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
```

all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

NsiI		BglII		EcoRI	
SeqDerMap	FngrPrnt	SeqDerMap	FngrPrnt	SeqDerMap	FngrPrnt
21251	20929	12417	12174	8696	8794
12148	11918	2067	2041	6	<800
199	<800	5666	5826	1775	1773
3275	3221	254	<800	2000	1991
20379	20929	3818	3836	6313	6324
15555	15150	747	735	3256	3226
675	<800	9196	9237	325	<800
5493	5475	4154	4101	12989	12723
516	<800	5820	5826	5955	5951
5810	5831	118	<800	611	<800
9488	9435	2524	2359	1995	1991
2908	2935	8844	8768	11945	12009
779	840	332	<800	5577	5593
821	840	564	<800	4139	4124
315	<800	26	<800	955	940
3640	3671	4675	4644	2961	2940
428	<800	1801	1803	5264	5205
1144	1119	117	<800	1535	1534
4684	4717	6797	6799	3313	3383
20	<800	3146	3177	3760	3761
492	<800	2376	2359	3061	3110
10935	10879	210	<800	9605	9505
5921	6010	5135	5110	335	<800
529	<800	744	735	2190	2194
4354	4384	881	947	5117	5205
1311	1293	413	<800	13558	13434
10	<800	6389	6456	9367	9505
374	<800	296	<800	8080	8019
1497	1480	7160	7119	4276	4243
4079	4083	4846	4822	7830	8019
337	<800	2914	2924	231	<800
4483	4384	3803	3836	533	<800
1530	1480	1832	1803	668	<800
249	<800	674	<800	12314	12009
8831	8995	2515	2513	18561	18820
244	<800	2163	2137	11006	11013
1019	1000	466	<800	8756	8794
841	840	927	947	7	<800
8114	8086	5963	5826		
9184	9435	7440	7660		
7121	7263	5159	4822		
1122	1119	677	<800		
49	<800	1399	1373		
11928	11918	1565	1554		
1499	1480	2388	2513		
2585	2575	4826	4822		
699	<800	7661	7660		
		3624	3705		
		8693	8768		
		1749	1803		
		1642	1635		
		5295	5362		
		10628	10715		
		3227	3177		
		589	<800		

Query Match 18.5%; Score 462.6; DB 8; Length 190162;
Best Local Similarity 61.3%; Pred. No. 1.3e-83;
Matches 900; Conservative 1; Mismatches 520; Indels 46; Gaps 8;

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Qy      604 TTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGT 663
            |||| ||| ||      |||| || | ||||||||  ||||||||||  | |  ||||
Db    31687 TTTTCCTTTTTTTAAAAGTAGAAACGGAGTCTTGCTGGGTCACCCAGGCTGGGGTGCAGT 31746

Qy      664 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 723
            |||||  | |   |||||||| ||| |  ||||  |  || | ||||  |  || |||
Db    31747 AGTGCAGTCGTGTTTCACTGCATCCTTCAATTCCTAGGAACAGGTGATCCTCCCACTTCA 31806
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Qy       724 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATT 783
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Qy       784 TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAA 843
Db     31867 TGTTTGAAGACACAGGGTCTTGCTGTGTTGCTCAGGCTGGTCTCAAACAGCCAGCCTCAA 31926

Qy       844 GCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 903
Db     31927 GTGATCCTCCTGCCTCATCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCATGCCC 31986

Qy       904 GGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGA 963
Db     31987 AGCCCATTTCTTTTTTCTGTTTTTTTTTTTAAATTTAATTTAATTTTTATTTTTTATTTT 32046

Qy       964 TTACTGCCTATTTTCTTCCTT-TCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACC 1022
Db     32047 TATTTTTATTTTTATTTATTTATTTTTTTTGAGATGAAGTCTCACTCTGTCGCCCAGGCT 32106

Qy      1023 TCCGT--------------TCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTC 1068
Db     32107 GGAGTGCAGTGGCATGATCTCGGCTCACTGAAACCTCTGCCTCCCAGGTTCAAGCGATTC 32166

Qy      1069 TCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAT 1128
Db     32167 TCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGCCCTCCACTATACCCGGCTAA- 32225

Qy      1129 TTTTTGTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCC 1188
Db     32226 TTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTAGTCAGGCTGGTCTCGAACTCC 32285

Qy      1189 TGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTC 1248
Db     32286 TGACCTCAGATGATCTGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCC 32345

Qy      1249 ACTGTGCCTGGCCGATTACTGTCTATTTT---CTTTATTGCTATATCCCCAGATCTAGAG 1305
Db     32346 ACCGCACCCGGCTGCCCCATTTTTTTTTTAAACAAATGCTTACTGACCTACGCTAAGAG 32405

Qy      1306 CAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATA 1365
Db     32406 CTGTAAGGGCAAATGAGACAATGTCCTTACCCTCAGAATCTTATATTTTGGTGAGATAAT 32465

Qy      1366 AACTTTCTTTTTCTTTTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTG 1425
Db     32466 ACACATATATAAATAATGATGATACAAGGACATATATAATAAATGCCATGACAGATTATA 32525

Qy      1426 CATTCTGCTTTTTCAC-TTATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTA 1484
Db     32526 AATCCATATTCACTACACAAACAAGAGGCTTAGGAAAGTTCAGATTCCCACTTTGGGAAG 32585

Qy      1485 TTGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTT 1544
Db     32586 CTGAGGCAGGTGGATCACCTGAGGTCAGGAATTCA--AGACCAGCGTGGCCAACATGGTG 32643

Qy      1545 ATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAAC 1604
Db     32644 AAACCCTGTCTTTACTAAGAGTACAAAAATTAGCTGAGTGTGGTGGTGCAGGCCTGTAAT 32703

Qy      1605 CCTCTCCCCAGAGAAATACACACACACACACACACTCACACACAGTTTTTTTTTAATGTT 1664
Db     32704 CCTAGCTACTCATGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCGGAGGCTGCA 32763

Qy      1665 TGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTG---------------------- 1702
Db     32764 GTGAGCCGAGATCGCGCCACTGCACTCTAGCCTGGGTGACAGAGTGAGACTCCATCTCAA 32823

Qy      1703 TTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGTAC 1762
Db     32824 AAAAAAAAAAAAAAAAAAAAAGAGGCCAGGCGCGGTGGCTCACACCTGTAATCCCAGCAC 32883

Qy      1763 TTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAA 1822
Db     32884 TTTGGGAGCCTGAGGTGGGCGGATCA--TGAGGTCAGAAGTTCGAGACCAGCCTGGCCAA 32941

Qy      1823 TATGGTGAAACCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGC 1882
Db     32942 TATGGTGAAACCCCGTCTTTACTAAAAGTACAAAAATTAGCTGGGCGTGGTGCCACGCAC 33001

Qy      1883 CTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGA 1942
Db     33002 CTGTAGTCCCAGCTACTCAGGAGGCTAAGGCAGGAGAATCGCTTGAACCCAGGAGGCAGA 33061

Qy      1943 GGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCT 2002
Db     33062 GGTTGCAGTGAGCCGAGATTATGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCC 33121

Qy      2003 ATCTCAAAAAAATAAATAAATAAAATA 2029
Db     33122 GTCTCAAAAAAAAAAAAGAAAAGAAAA 33148
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RESULT 8
AP000589

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LOCUS       AP000589              123192 bp    DNA     linear   HTG 30-MAY-2000
DEFINITION  Homo sapiens chromosome 11 clone CMB9-105N5 map 11q13, WORKING
            DRAFT SEQUENCE, 19 unordered pieces.
ACCESSION   AP000589
VERSION     AP000589.3  GI:8118795
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 123192)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens 123,192 genomic DNA of 11q13
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 123192)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-OCT-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
COMMENT     On May 31, 2000 this sequence version replaced gi:6997479.
            -------------- Genome Center
                Center: RIKEN Genomic Sciences Center(GSC)
                Center code: RIKEN
                Web site: http://hgp.gsc.riken.go.jp/
                Contact: hattori@gsc.riken.go.jp
            -------------- Project Information
                Center project name: HumDraft11
                Center clone name: CMB9-105N5
            -------------- Summary Statistics
                Sequencing vector: PCR products; 100% of reads
                Chemistry: Dye-terminator ET-amersham; 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 115116 bases at least Q40
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                Consensus quality: 120191 bases at least Q20
                Insert size: 121392; sum-of-contigs
                Quality coverage: 5.08x in Q20 bases; sum-of-contigs
            --------------.
            NOTE: This is a 'working draft' sequence. It currently consists of
            19 contigs. The true order of the pieces is not known and their
            order in this sequence record is arbitrary. Gaps between the
            contigs are represented as runs N, but the exact sizes of the gaps
            are unknown. This record will be updated with the finished sequence
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as soon as it is available and the accession number will be
preserved
         1     15827 contig of  15827 bp in length
     15928     30484 contig of  14557 bp in length
     30585     40602 contig of  10018 bp in length
     40703     51912 contig of  11210 bp in length
     52013     60022 contig of   8010 bp in length
     60123     70438 contig of  10316 bp in length
     70539     77945 contig of   7407 bp in length
     78046     85717 contig of   7672 bp in length
     85818     92399 contig of   6582 bp in length
     92500     98215 contig of   5716 bp in length
     98316    104148 contig of   5833 bp in length
    104249    109166 contig of   4918 bp in length
    109267    112457 contig of   3191 bp in length
    112558    115076 contig of   2519 bp in length
    115177    117063 contig of   1887 bp in length
    117164    118652 contig of   1489 bp in length
    118753    120425 contig of   1673 bp in length
    120526    121843 contig of   1318 bp in length
    121944    123192 contig of   1249 bp in length
Sequence updated (18-Oct-1999)
Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*         1     15827: contig of 15827 bp in length
*     15828     15927: gap of 100 bp
*     15928     30484: contig of 14557 bp in length
*     30485     30584: gap of 100 bp
*     30585     40602: contig of 10018 bp in length
*     40603     40702: gap of 100 bp
*     40703     51912: contig of 11210 bp in length
*     51913     52012: gap of 100 bp
*     52013     60022: contig of 8010 bp in length
*     60023     60122: gap of 100 bp
*     60123     70438: contig of 10316 bp in length
*     70439     70538: gap of 100 bp
*     70539     77945: contig of 7407 bp in length
*     77946     78045: gap of 100 bp
*     78046     85717: contig of 7672 bp in length
*     85718     85817: gap of 100 bp
*     85818     92399: contig of 6582 bp in length
*     92400     92499: gap of 100 bp
*     92500     98215: contig of 5716 bp in length
*     98216     98315: gap of 100 bp
*     98316    104148: contig of 5833 bp in length
*    104149    104248: gap of 100 bp
*    104249    109166: contig of 4918 bp in length
*    109167    109266: gap of 100 bp
*    109267    112457: contig of 3191 bp in length
*    112458    112557: gap of 100 bp
*    112558    115076: contig of 2519 bp in length
*    115077    115176: gap of 100 bp
*    115177    117063: contig of 1887 bp in length
*    117064    117163: gap of 100 bp
*    117164    118652: contig of 1489 bp in length
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*    118753    120425: contig of 1673 bp in length
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*    120526    121843: contig of 1318 bp in length
*    121844    121943: gap of 100 bp
*    121944    123192: contig of 1249 bp in length.
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                     /note="assembly_fragment"
ORIGIN

  Query Match            18.4%;  Score 460.6;  DB 14;  Length 123192;
  Best Local Similarity   59.8%;  Pred. No. 3.5e-83;
  Matches  882;  Conservative    1;  Mismatches  575;  Indels   17;  Gaps    6;

Qy        598 TTTGGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTC-TGTCACCCAGGCATGA 656
              |||   ||||||||| || || ||| ||||||| || |  ||| |||  |||||||  ||
Db      63120 TTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTTTCTCTCTTGTTGCCCAGGCTGGA 63179

Qy        657 GCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCT 716
              |  || |||  ||| |   | ||||  || ||||  ||||| | | |||||||  |   |
Db      63180 GTGCAATGGCACAATCTCGGTTCACCACAACCTCCGCCTCCCGGGTTCAAGGGTTTCTCC 63239

Qy        717 GACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAA 776
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Db      63240 TGCCTCAGCCTCCCGAGTAGCTGAGATTACAGGCATGCGCCACCACGCCCAGCTGATTTT 63299

Qy        777 AAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTG 836
              |   || || |||||||| |||| |  | | ||||| |||||| ||||  | ||||||
Db      63300 GTA---TTATTAGTAGAGACGGGGTTTCTCCATGTTGGTCAGGCTGGTCTCGAGCTCCTG 63356

Qy        837 GCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCAC 896
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Db      63357 ACCTCAGGTGATCCACCCACCTCGGCCTCCCAAAGTGCTGGGATTATAGGTGTGAGCCAT 63416

Qy        897 CATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGA 956
              || |  |||| |  || |  |||  |     ||  ||    || |          |
Db      63417 CACGCCCGGCCTCACATATTCTTATCCTAATATGTTTTCATGCTTTGAAGTCCTACAGTA 63476

Qy        957 ACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACC 1016
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Db      63477 ATCATCCTTTGATTCTTTTTTTTTGAGACAGTCTTGCTCTGTCCACCAGGCTGGAGTGCA 63536

Qy       1017 TCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCT 1076

Db      63537 ATGGCGCAATCTCGGCTCACTGCAAACTCTGCCTCCGAGGTTCACGCGATTCTCCTGCCT 63596

Qy       1077 AAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTT--G 1134

Db      63597 CAGCCTCCAGAGTAGCTGGGATTACAGGTGCGCGCCACCACGTCTGGCTACTTTTTTTGT 63656

Qy       1135 TATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCT 1194

Db      63657 ATTTTTTAGTAGAGACAGGGTTTCACCATGTTGGTCAGGCTGGTCTCGAACTCCTGACCT 63716

Qy       1195 CAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTG 1254

Db      63717 CAGGTGATCCGCCTGCCTCAGCCTTCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCG 63776

Qy       1255 CCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTG 1314

Db      63777 CCCGATGCCCTTTGATTCTTTGAAACAAAATGTATATAAATTAAAATGCTAAAACGT-TA 63835

Qy       1315 ACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTT 1374

Db      63836 TCATTTCCTGTGATCATAAGGCTCTGACAACATTTTCCTCTAGATTATGTTGTCATTATG 63895

Qy       1375 TTTCTTTTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCT 1434

Db      63896 ATTATTATTCACACATAAAGCAAAATAATATGGGTACTACAAATTTTGATGCTATTTATT 63955

Qy       1435 TTTTCA---------CTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTAT 1485

Db      63956 ATATCAATATAAAGGATGATTAGCCAGAGAAAACTAAATGTTATTGGAAAGGTATCTGAA 64015

Qy       1486 TGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTA 1545

Db      64016 TGGGTGTTTAGGTTTTCCCTCTCACTTAGTTAACATACCCAGAGATGGATATTATTTGT 64075

Qy       1546 TACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACC 1605

Db      64076 TTCTAGAACAAGACAGGAATTAGCATCCTGTTTTCATTTTTATAGATATGACCACTGAGT 64135

Qy       1606 CTCTCCCCAGAGAAATACACACACACACACACACTCACACACAGT-TTTTTTTTAATGTT 1664

Db      64136 CCATGGAGCTAGAAGGAATTTGTTAGAGTGAATTTTCCCAACTCTGTCCAAGTTGGAGGC 64195

Qy       1665 TGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAAAAATAACT 1724

Db      64196 CAAAAATGTCACAATGTAATCTAGAGTCAAATTATTTTTTACTTTTTAAAATGATGTTGA 64255

Qy       1725 CAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGG 1784

Db      64256 AGGCCAGGTGGGGTGGCTCACGTATGTAATCCAAGCACTTTGGAAGGCCGAGGCAGGTGG 64315

Qy       1785 ATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTAC 1844

Db      64316 ATTACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACACTGTCTCTAC 64375

Qy       1845 TAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGA 1904

Db      64376 TAAAAATACAAAAATTAGCTGGGCGTGGTGATGCGTGCCTGTAATCCCAGCTACTTGGGA 64435

Qy       1905 GGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCC 1964

Db      64436 GGCTGAGGCAGAAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATTGT 64495

Qy       1965 ACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATA 2024

Db      64496 GTCACTGCACTCCAGCCTGGGCAACAGACCAAGATTCTGTCTCAAAATAAATAATAAATA 64555

Qy       2025 AAATAAAGGATCGGAGAGAAACAAAACTAATAAGA 2059

Db      64556 AAAATAATGAAAATAATAAAATGATGTTAAAGATA 64590
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RESULT 9
AC022408
LOCUS       AC022408               150266 bp    DNA     linear   PRI 21-AUG-2001
DEFINITION  Homo sapiens chromosome 15 clone RP11-118J16 map 15q15, complete
            sequence.
ACCESSION   AC022408
VERSION     AC022408.6  GI:15217198
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 150266)
  AUTHORS   Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
            Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
            Pate,D. and Hood,L.
  TITLE     Sequencing of human chromosome 15 D15S146-D15S117 region
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 150266)
  AUTHORS   Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
            Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
            James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
            and Hood,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-FEB-2000) Multimegabase Sequencing Center, University
            of Washington, PO BOX 357730, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 150266)
  AUTHORS   Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
            Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
            Pate,D. and Hood,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-2001) Multimegabase Sequencing Center, Institute
            for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
            98105, USA
COMMENT     On Aug 21, 2001 this sequence version replaced gi:11225361.
            ------------ Genome Center
                Center: Multimegabase Sequencing Center
                Center code: UWMSC
                Web site: http://chroma.mbt.washington.edu/msg_www
                Contact: leerowen@systemsbiology.org
            ------------ Summary Statistics
                Sequencing vector: pUC18; L08752
                Chemistry: Dye-terminator Big Dye; 90% of reads
                Chemistry: Dye-primer Big Dye; 10% of reads
                Assembly program: Phrap; version 0.990399
                Note:data from AC021753 [Drafting center UWMSC] and AC012652
            [Drafting center UWMSC] and 580I7 [Drafting center WUGSC] were
            added for finishing.
FEATURES             Location/Qualifiers
     source          1. .150266
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="15"
                     /map="15q15"
                     /clone="RP11-118J16"
                     /clone_lib="RPCI human BAC library 11"
                     /note="This clone overlaps RP11-46M12 AC012652 and
                     RP11-129I12 AC021753 and RP11-580I7 AC068981.Data from
                     overlapping BACs were combined and the consensus sequence
                     determined from RP11-118J16."
     misc_feature    1. .150266
                     /note="overlap with RP11-580I7 AC068981."
     misc_feature    1. .100397
                     /note="overlap with RP11-129I12 AC021753."
     unsure          49355. .49359
                     /note="low quality data."
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                     /note="overlap with RP11-46M12 AC012652."
ORIGIN
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Query Match 18.4%; Score 460.4; DB 8; Length 150266;
Best Local Similarity 62.0%; Pred. No. 3.7e-83;
Matches 889; Conservative 1; Mismatches 487; Indels 57; Gaps 8;

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Qy        600 TGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCA 659
Db      52138 TGTGTATTTTGTTGTTGTTGTTGTTGAGCCAGCTCGGGCTCTGTCGCCCAGGCTGGAGTG 52197

Qy        660 CAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGAC 719
Db      52198 CAGTGGCTCGATCTCGGCTCACTGCAATCTCTGCCTCCTGGGCTCAAGCCATCCTCTCAC 52257

Qy        720 CTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAA 779
Db      52258 CTCAGCATCCCAAGTAGCTGGGACTACAGGTGCACATCACCATGCTTAGCTAATTTTTGT 52317

Qy        780 AATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCT 839
Db      52318 A--TTTTCTGTAGAGACAGGGTTTTGCCATGTTGCCCATGCTGATTTCAAACTCCTGAGC 52375

Qy        840 TCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCAT 899
Db      52376 TCAAACGATCCGCCT-GCTCAGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCAA 52434

Qy        900 GTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACA 959
Db      52435 GCCTAACCTATTTAATGTGAATTTGTATGTTGGCATATAAAATCCCCTAGCCAGTTTTGT 52494

Qy        960 GGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCA 1019
Db      52495 TTTGTT-TTGTTTTTTTGAGACAGAGTTTTGCTCTTGTTGCACTCCACTGGAGTGCAGTG 52553

Qy       1020 ACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAG 1079
Db      52554 GCTCAATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAG 52613

Qy       1080 CCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTT 1139
Db      52614 CCTCCTGAGTAGCTGGGATTACAGGTGCGCGCCACCACGCCCAGCTAATTTTTTGTATTT 52673

Qy       1140 TTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGT 1199
Db      52674 TTGGTAGAGTCAGAGTTTAACCATGTTGGCCAGGCTGGTTTCGAACTCCTGACCTCAGGT 52733

Qy       1200 GATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGG 1259
Db      52734 GATCCACCTGCCTCAGTCTCCCAAAGTGCAGGGATTACAGGCGTGAGCCACCGCACCCGG 52793

Qy       1260 CCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATA 1319
Db      52794 CCAACAAACTTTCATTAAGTGAACCTCTAACACCACAGCTTATAATTAGTTT-------- 52845

Qy       1320 TAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCT 1379
Db      52846 -------------TGTTTTGTTTTTAGAGACAGGGTCTCGCTCTCCACCCAGGCTTGAG 52891

Qy       1380 TTTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTC 1439
Db      52892 TGCGCTGGCACAATCATAGCTCACTAGGGACTCAA--------------------GTGA 52930

Qy       1440 ACTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTT 1499
Db      52931 TCCTCTTGCCTCCTGAGTAACTGGGACTACAGGCTTGAGACACCATGCCCAGCAGAATAG 52990

Qy       1500 CATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCT 1559
Db      52991 CTCTCGATTTGTTGCTTTGGCTTAATCACATTTCCACCTTGATGTACTCAAAATGTTTTT 53050

Qy       1560 CCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGAGAA 1619
Db      53051 ATTAGTCATA-----AACTTTTCTAATCACATTTGTGCTCACTACAATTATTTCCTATCA 53105

Qy       1620 ATACACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAG 1679
Db      53106 CAATTTACAGACTTTCAAAAATTGATTTGGTTTCTACTGAAATAAAACGTAGAGGAAAAG 53165

Qy       1680 AAACCTGCA---TTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACA 1736
Db      53166 AACACAGTAAGCTAAAATGATGGAATTCAATCCCTTAAAAACAAAATTCAGCCGGGCACG 53225

Qy       1737 GTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGT 1796
Db      53226 GTGGCTCACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGTAGGTGGATCAC--GAGGT 53283

Qy       1797 GAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAA 1856
Db      53284 CAGGGGCTCGAGACCAGCCTGACCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAA 53343

Qy       1857 AATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAG 1916
Db      53344 AATTAGCTGGGTGTGGTGGCGGGCGCCTGTAATACCAGCTACTCAGGAGGCTGAGGCAGG 53403

Qy       1917 AGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTC 1976
Db      53404 AGAATTGCTTGAACCCGGGAGGCGGAAGCTGCAGTGAGCCGAGATCACACCACTATACTC 53463

Qy       1977 CAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATAA 2030
Db      53464 CAGCCTGGGCGACAGAGCCAGACTCCGTCTCAAAAAACAAAAAAAAAACATTCA 53517
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RESULT 10
AC021753

LOCUS	AC021753 167996 bp DNA linear PRI 29-OCT-2001
DEFINITION	Homo sapiens chromosome 15 clone RP11-129I12 map 15q15, complete sequence.
ACCESSION	AC021753
VERSION	AC021753.7 GI:16507213
KEYWORDS	HTG.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 167996)
AUTHORS	Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R., Pate,D. and Hood,L.
TITLE	Sequencing of human chromosome 15 D15S146-D15S117 region
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 167996)
AUTHORS	Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T. and Hood,L.
TITLE	Direct Submission
JOURNAL	Submitted (20-JAN-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA
REFERENCE	3 (bases 1 to 167996)
AUTHORS	Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R., Pate,D. and Hood,L.
TITLE	Direct Submission
JOURNAL	Submitted (29-OCT-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA
COMMENT	On Oct 29, 2001 this sequence version replaced gi:11136698. ---------- Genome Center Center: Multimegabase Sequencing Center Center code: UWMSC Web site: http://chroma.mbt.washington.edu/msg_www Contact: leerowen@systemsbiology.org ---------- Summary Statistics Sequencing vector: pUC18; L08752 Chemistry: Dye-terminator Big Dye; 90% of reads

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            Chemistry: Dye-primer Big Dye; 10% of reads
            Assembly program: Phrap; version 0.990399
            Note: data from AC022408 [Drafting center UWMSC] and AC020661
          were added for fimishing.
FEATURES             Location/Qualifiers
     source          1. .167996
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="15"
                     /map="15q15"
                     /clone="RP11-129I12"
                     /clone_lib="RPCI Human BAC library 11"
                     /note="This clone overlaps RP11-118J16 AC022408 and
                     RP11-540O11 AC020661. Data from overlapping BACs were
                     combined and the consensus sequence determined from
                     RP11-129I12 to the extent possible."
     misc_feature    1. .63402
                     /note="overlap with RP11-540O11 AC020661."
     misc_feature    67596. .167996
                     /note="overlap with RP11-118J16 AC022408."
ORIGIN

  Query Match             18.4%;  Score 459.4;  DB 8;  Length 167996;
  Best Local Similarity   62.0%;  Pred. No. 5.8e-83;
  Matches  888;  Conservative    1;  Mismatches  487;  Indels   57;  Gaps    8;

Qy        600 TGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCA 659
Db     119755 TGTGTATTTTGTTGTTGTTGTTGTTGAGCCAGCTCGGGCTCTGTCGCCCAGGCTGGAGTG 119814

Qy        660 CAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGAC 719
Db     119815 CAGTGGCTCGATCTCGGCTCACTGCAATCTCTGCCTCCTGGGCTCAAGCCATCCTCTCAC 119874

Qy        720 CTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAA 779
Db     119875 CTCAGCATCCCAAGTAGCTGGGACTACAGGTGCACATCACCATGCTTAGCTAATTTTTGT 119934

Qy        780 AATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCT 839
Db     119935 A--TTTTCTGTAGAGACAGGGTTTTGCCATGTTGCCCATGCTGATTTCAAACTCCTGAGC 119992

Qy        840 TCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCAT 899
Db     119993 TCAAACGATCCGCCT-GCTCAGCCTCCCAAAGTGCCGGGATTACAGGTGTGAGCCACCAA 120051

Qy        900 GTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACA 959
Db     120052 GCCTAACCTATTTAATGTGAATTTGTATGTTGGCATATAAAATCCCCTAGCCAGTTTTGT 120111

Qy        960 GGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCA 1019
Db     120112 TTTGTT-TTGTTTTTTTGAGACAGAGTTTTGCTCTTGTTGCACTCCACTGGAGTGCAGTG 120170

Qy       1020 ACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAG 1079
Db     120171 GCTCAATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAG 120230

Qy       1080 CCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTT 1139
Db     120231 CCTCCTGAGTAGCTGGGATTACAGGTGCGCGCCACCACGCCCAGCTAATTTTTTGTATTT 120290

Qy       1140 TTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGT 1199
Db     120291 TTGGTAGAGTCAGAGTTTAACCATGTTGGCCAGGCTGGTTTCGAACTCCTGACCTCAGGT 120350

Qy       1200 GATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGG 1259
Db     120351 GATCCACCTGCCTCAGTCTCCCAAAGTGCAGGGATTACAGGCGTGAGCCACCGCACCCGG 120410

Qy       1260 CCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATA 1319
Db     120411 CCAACAAACTTTCATTAAGTGAACCTCTAACACCACAGCTTATAATTAGTTT-------- 120462

Qy       1320 TAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCT 1379
Db     120463 --------------TGTTTTGTTTTTAGAGACAGGGTCTCGCTCTCCACCCAGGCTTGAG 120508

Qy       1380 TTTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTC 1439
Db     120509 TGCGCTGGCACAATCATAGCTCACTAGGGACTCAA--------------------GTGA 120547

Qy       1440 ACTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTT 1499
Db     120548 TCCTCTTGCCTCCTGAGTAACTGGGACTACAGGCTTGAGACACCATGCCCAGCAGAATAG 120607

Qy       1500 CATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCT 1559
Db     120608 CTCTCGATTTGTTGCTTTGGCTTAATCACATTTCCACCTTGATGTACTCAAAATGTTTTT 120667

Qy       1560 CCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGAGAA 1619
Db     120668 ATTAGTCATA-----AACTTTTCTAATCACATTTGTGCTCACTACAATTATTTCCTATCA 120722

Qy       1620 ATACACACACACACACACACTCACACACAGTTTTTTTTAATGTTTGCAACTAAGACAAG 1679
Db     120723 CAATTTACAGACTTTCAAAAATTGATTTGGTTTCTACTGAAATAAAACGTAGAGGAAAAG 120782

Qy       1680 AAACCTGCA---TTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACA 1736
Db     120783 AACACAGTAAGCTAAAATGATGGAATTCAATCCCTTAAAAACAAAATTCAGCCGGGCACG 120842

Qy       1737 GTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGT 1796
Db     120843 GTGGCTCACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGTAGGTGGATCAC--GAGGT 120900

Qy       1797 GAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAA 1856
Db     120901 CAGGGGCTCGAGACCAGCCTGACCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAA 120960

Qy       1857 AATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAG 1916
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Qy       1917 AGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTC 1976
Db     121021 AGAATTGCTTGAACCCGGGAGGCGGAAGCTGCAGTGAGCCGAGATCACGCCACTATACTC 121080

Qy       1977 CAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATA 2029
Db     121081 CAGCCTGGGCGACAGAGCCAGACTCCGTCTCAAAAAACAAAAAAAAAAAACA 121133
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RESULT 11
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LOCUS       AC003689              137693 bp    DNA     linear   PRI 21-NOV-1998
DEFINITION  Homo sapiens Chromosome 11q12.2 PAC clone pDJ1081b4 containing
            human mRNA for T-cell glycoprotein CD6, complete sequence.
ACCESSION   AC003689
VERSION     AC003689.1  GI:3900834
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 137693)
  AUTHORS   Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
            Buettner,J., Bumeister,R., Card,P., deSailboat,F., Dunn,J.,
            English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
            Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,
            Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
            Schageman,J., Schultz,R.A., Stimson,S., Syed,M. and Ward,T.
  TITLE     HTGS Submission
  JOURNAL   Unpublished
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REFERENCE   2  (bases 1 to 137693)
  AUTHORS   Evans,G.A., Athanasiou,M., Basit,M., Bradbury,P., Brignac,S.,
            Bumesiter,R., Davis,C., English,C., Franklin,T.L., Garner,H.R.,
            Gee,V., Gordon,M., Gotway,G., Grant,O., Hahner,L., Harris,J.,
            Hinson,S., Narayanaswamy,U., Newton,J., O'Brien,K., Patel,P.,
            Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D.,
            Ward,T. and Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1997) Genome Science & Technology Center,
            University of Texas Southwester Medical Center, 5323 Harry Hines
            Blvd, Dallas, TX 75235-8591, USA
REFERENCE   3  (bases 1 to 137693)
  AUTHORS   Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
            Buettner,J., Butler,C., Card,P., deSailboat,F., Dunn,J.,
            English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
            Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,
            Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
            Schageman,J., Schultz,R.A., Stimson,S., Waller,K. and Ward,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-1998) Genome Science & Technology Center,
            University of Texas Southwestern Medical Center, 5323 Harry Hines
            Blvd, Dallas, TX 75235-8591, USA
COMMENT     On Nov 21, 1998 this sequence version replaced gi:2695567.
            Further information regarding the map of this region or
            annotation of pDJ1081b4 can be found at
            http://gestec.swmed.edu/chromoso1.htm
            IMPORTANT: This submission contains the entire insert of clone
            pDJ1081b4.  pDJ1081b4 comes from the RPCI-3 PAC library constructed
            at the Roswell Park Cancer Institute by the Pieter de Jong group.
            This clone has been finished according to strict quality criteria
            and attempts have been made to resolve all base calling problems
            such as compressions and repetitive elements.  The expected
            Phred/Phrap calculated errors/10kb is 0.98.  In addition, attempts
            have been made to assure over 99% of consensus base calls consist
            of either double-stranded coverage or 2 types of labeling chemistry
            on one strand.
            CHROMOSOMAL LOCUS: This PAC clone comes from the Chromosome
            11p12.2 Best's disease region mapped between STS D11S461 and EST
            AHNAK.  This region spans over 1.5 Mbp.
            MARKER CONFIRMATION: ESTs/STSs sequence confirmed; CD6, D11S461
            MAPPED CLONE OVERLAP: PACs pDJ606g6 and pDJ59L21.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     repeat_region   164. .454
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Qy       1375 TTTCTTTTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCT 1434
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Qy       1965 ACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATA 2024
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DEFINITION  Homo sapiens genomic DNA, chromosome 11 clone:RP11-881M11, complete
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ACCESSION   AP003721
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            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA
  JOURNAL   Published Only in Database (2001)
REFERENCE   2  (bases 1 to 201460)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     On Jun 16, 2003 this sequence version replaced gi:28189463.
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  Best Local Similarity   59.7%;  Pred. No. 2.5e-82;
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Qy       1971 GCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATAA 2030
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ACCESSION   AC116933
VERSION     AC116933.2  GI:27356688
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Papio anubis (olive baboon)
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            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 195986)
  AUTHORS   Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
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            Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,
            Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 195986)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-APR-2002) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
REFERENCE   3  (bases 1 to 195986)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-2002) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     On Dec 21, 2002 this sequence version replaced gi:19909407.
            ---------- Genome Center
                 Center: NIH Intramural Sequencing Center
                 Center code: NISC
                 Web site: http://www.nisc.nih.gov
                 Contact: nisc_zoo@nhgri.nih.gov
            ---------- Project Information
                 Center project name: cqw
                 Center clone name: 001C24

            The sequence data in this record represents an 'enhanced'
            version of a Phase 2 submission. Specifically, the indicated
            order and orientation of each sequence contig has been
            established using one or more of the following: read-pair
            data from individual subclones, overlaps with neighboring
            clones, alignment with available reference sequence (e.g.,
            human), and/or confirmation by PCR testing. In addition,
            the sequence assembly is based on at least 8X average
            coverage in Q20 bases and has been reviewed to rule out
            gross misassemblies, the low-quality ends of sequence
            contigs have been trimmed away, and each base is associated
            with a Phrap-derived quality score.
            ---------- Summary Statistics
                 Sequencing vector: plasmid; n/a; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990319
                 Consensus quality: 195122 bases at least Q40
                 Consensus quality: 195370 bases at least Q30
                 Consensus quality: 195594 bases at least Q20
                 Insert size: 186000; agarose-fp
                 Insert size: 195686; sum-of-contigs
                 Quality coverage: 9.19x in Q20 bases; agarose-fp
                 Quality coverage: 8.74x in Q20 bases; sum-of-contigs
            ----------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1    76152: contig of 76152 bp in length
            *   76153    76252: gap of unknown length
            *   76253   126668: contig of 50416 bp in length
            *  126669   126768: gap of unknown length
            *  126769   177394: contig of 50626 bp in length
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Db     180502 TTTTCCTTTTTTTTTAAGTAGAGACAGAGTCTTGCTCTGTCACCCAGGCTGGAGTGCAGT 180561

Qy        664 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 723
              ||||||   |   || ||||| ||| | ||||| |  || | ||||  |  ||||||
Db     180562 AGTGCAATAGTGTTTCCCTGCATCCTTCAATTCCTGGGAACAGGTGATCCTCCCACCTCA 180621

Qy        724 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATT 783
              | || |  |||||||||||||    ||      |||||| |||  ||||| | ||||||||
Db     180622 GTCTTCTGAGTAGCTGGGACTTTAGGCACATGCCACCATGCCCAGCTAACTTAAAAAATT 180681

Qy        784 TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAA 843
              |||||| ||| || |||||||  ||  ||||  ||||||  |||  ||||  | ||| ||||
Db     180682 TTTTTGAAGACACAGGGTCTTGCTCTGTTGCTCAGGCTACTCTCAAACAGCCGGCCTCAA 180741

Qy        844 GCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 903
              |  ||||||   |||   | |||||||||||||||||| ||| ||||||||||||  |
Db     180742 GTGATCCTCTCGCCTCATCCTCCCAAAGTGCTGGGATTAGAGGTGTGAGCCACCATGCCC 180801

Qy        904 GGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGA 963
              ||   || ||| || |  |   |  ||          | |||  |  |          |
Db     180802 AGCCCATTTTTTTTTAATTTCTTAATTTAATTTCTATTTTTAATTTTTA---TTATTTTA 180858

Qy        964 TTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCT 1023
              ||| |      |||  ||  ||   |||||||||||||||||| | ||| |      |
Db     180859 TTATTTTTATTTTATTTATTTATATTTTTGAGACAGAGTCTCACTCCGTCGCACAGGCTG 180918

Qy       1024 CCGT--------------TCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCT 1069
                ||              |||||||||||||||| ||||||||||||||: | ||
Db     180919 GAGTGCAATGGTGTGATCTCAGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCAACTCC 180978

Qy       1070 CCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATT 1129
              ||||||| |||||||||||||||||| |||||| | |  | |||| |  | ||||||| |
Db     180979 CCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGGCCTCCACTACACCTGGCTAA-T 181037
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Qy       1130 TTTTGTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCT 1189
             ||||||||||||||| ||||| ||||||| ||||||||   |||||||||| |||||||
Db     181038 TTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTAGTCAGGCTGGTCTTGAACTCCT 181097

Qy       1190 GACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCA 1249
             ||||||| |||| | |||||||| | ||||||||||||||| |||| ||||||||| ||
Db     181098 GACCTCAGGTGACCCGCCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCA 181157

Qy       1250 CTGTGCCTGGCCGATTACTGTCTATTTTCT----------TTATTGCTATATCCCCAGAT 1299
             ||||||| ||       | ||| |||| |          ||| |    ||  |  |||
Db     181158 CTGTGCCCAGCAACCCCATTTCTTTTTTTTAAACAAATGCTTACTAACCTACTCTAAGAG 181217

Qy       1300 CTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTA 1359
             ||  |   |   |||  |  ||  | | |   |||  |   |   |   |
Db     181218 CTGTAAGGGCAAATGAGGCAATGTCTTTACCCTCAGAATCTTATCTTTTGGTGAGGAGAT 181277

Qy       1360 GATATAAACTTTCTTTTTCTTTTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACA 1419
              ||| | |  |   |  |  |   | |||   ||| || |    ||   | || |
Db     181278 AATACACATATATAAATAATGATACAAGGACATATATGATAAATGCCATGACAGATTATA 181337

Qy       1420 ATCTTGCATTCTGCTTTTTCACTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAAC 1479
             |      ||||        |      | ||    | |  ||    ||||| ||| || |
Db     181338 AATCCATATTCAC-----TACACAAACAAGAGGCTTAGAAAAGTTCAGATTCCCACTTTG 181392

Qy       1480 CTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATT 1539
                | || | |   |||       |        |||   |  |   |   ||
Db     181393 GGAGGCCGAGACAGGTGGATCACCTGAGGTCAGGAGTTCA--AGAGCAGCGTGGCCAACA 181450

Qy       1540 TGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTA 1599
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Db     181451 TGGTGAAACTCCGTCTCTACTAAAAGTACAAAAATTAGCCGGGGGTAGTGGAGGGCACCT 181510

Qy       1600 TGAACCCTCTCCCCAGAGAAATACACACACACACACACACTCACACACAGTTTTTTTTTA 1659
               || ||   |  |  ||||          | |  | ||   || |||
Db     181511 GTAATCCCAGCTACTCAGAAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCAGAGG 181570

Qy       1660 ATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGT---------------T 1704
               ||     | |  |||     |   ||||| |  ||  ||  |               |
Db     181571 CTGCAGTGAGCCGAGATTGCACCACTGCACTCTAGCCTGGGGGACAGAGCCAGACTCCAT 181630

Qy       1705 CATATTAATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACTT 1764
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Db     181631 CTCAAAAAAAAAAAAAAAAAAGGCCGGGCGCAGTGGCTCACACCTGTAATCCCAGCACTT 181690

Qy       1765 TGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATA 1824
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Qy       1825 TGGTGAAACCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCT 1884
             ||||||||||  |||||||||||||||||||||||||||||| || |||   |   |||
Db     181749 TGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGCCACGCACCT 181808

Qy       1885 GTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGG 1944
             ||||||||||||||||  ||||| |||||| ||||||  | ||||||  |||||  ||||
Db     181809 GTAGTCCCAGCTACTCAAGAGGCCGAGGCAGGAGAATCACCTGAACCCAGGAGGTGGAGG 181868

Qy       1945 TTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTAT 2004
             |||||||||||||| ||    ||| |||||||||||||||| | || ||||||||| ||
Db     181869 TTGCAGTGAGCCGAAATGGTGCCATTGCACTCCAGCCTGGGTGTCAGAGCGAGACTCCAT 181928

Qy       2005 CTCAAAAAAATAAATAAA 2022
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Db     181929 CTCAAAAAGAAAAAGAAA 181946
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RESULT 14
AC005052/c
LOCUS       AC005052              134210 bp    DNA     linear   PRI 08-NOV-2000
DEFINITION  Homo sapiens BAC clone CTB-38K21 from Xq23, complete sequence.
ACCESSION   AC005052
VERSION     AC005052.2  GI:10122134
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 134210)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
   PUBMED   9847074
REFERENCE   2  (bases 1 to 134210)
  AUTHORS   Tin-Wollam,A., Graves,T. and Cofman,M.
  TITLE     The sequence of Homo sapiens BAC clone CTB-38K21
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 134210)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 134210)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 134210)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-NOV-2000) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Sep 14, 2000 this sequence version replaced gi:3212939.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_RG038K21
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            This sequence was generated from part of bacterial clone contigs of
            human chromosome X, constructed by the chromosome X mapping group
            at the Sanger Centre, Wellcome Trust Genome Campus, Hinxton, UK.
            Further information can be found at
            http://www.sanger.ac.uk/HGP/ChrX/

            SOURCE INFORMATION:
            Clone CTB-38K21 is from the first release of the human BAC library
            CITB-978SK-B.  The library contains cloned DNA from the male
            fibroblast cell line 978SK.  See:  Shizuya et al., Proc. Natl.
            Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8
            (1996).  This clone is available from Research Genetics, Inc.
            (http://www.resgen.com).
            VECTOR:  pBeloBAC11
            Selection:  chloramphenicol

            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the right is RP3-327A19, 200 base pair
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          overlap.  Actual start of this clone is at base position 1 of
          CTB-38K21; actual end is at base position 9416 of RP3-327A19.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq23"
                     /clone="CTB-38K21"
                     /clone_lib="CITB-978SK-B"
     repeat_region   20. .268
                     /rpt_family="Alu"
     repeat_region   269. .561
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     repeat_region   978. .1285
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     misc_feature    2964. .4303
                     /note="CpG_island (%GC=68.3, o/e=0.70, #CpGs=110)"
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     repeat_region   6613. .6919
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     repeat_region   7154. .7214
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     repeat_region   8152. .8333
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     repeat_region   8565. .8749
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     repeat_region   8750. .9044
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     repeat_region   10238. .10290
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     repeat_region   10291. .10585
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     repeat_region   11310. .11544
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     repeat_region   12405. .12520
                     /rpt_family="L1"
     repeat_region   12712. .13008
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     repeat_region   13009. .13315
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     repeat_region   13603. .13850
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     repeat_region   13851. .14147
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     repeat_region   14223. .14526
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     repeat_region   14815. .15244
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     repeat_region   15245. .15566
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     repeat_region   17179. .17251
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     repeat_region   17255. .17390
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     repeat_region   17872. .18165
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     repeat_region   18239. .18532
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     repeat_region   18540. .18841
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     misc_feature    18631. .18876
                     /note="similar to  EST AW867673 (NID:g8001829)"
     repeat_region   19286. .19570
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     repeat_region   19885. .20185
                     /rpt_family="Alu"
     repeat_region   21149. .21446
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     repeat_region   21559. .21803
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     misc_feature    23875. .23924
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     misc_feature    23875. .23924
                     /note="similar to  EST AW619972 (NID:g7326156)"
     misc_feature    23878. .23926

  Query Match             18.0%;  Score 449.2;  DB 8;  Length 134210;
  Best Local Similarity   59.5%;  Pred. No. 6.9e-81;
  Matches  896;  Conservative    1;  Mismatches  554;  Indels   55;  Gaps    6;

Qy        555 TGAGCTATTTGCCCAAGATCACACAGCTTGTAAGTGGTGACAGTTTGGGTTTTTTTTTGT 614
              || | |||||||   | |         | |   |||| |  |  ||    ||| ||| |
Db      53793 TGTGGTATTTGCTTTATTTATTTATTTATTTTTTGGTTAGGGGGTGCTGATTTCTTTTT 53734

Qy        615 TGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTGGTGCAACCAT 674
              | || ||| |||||||||||||| ||||||||||||||  |||  |||||   | | |||
Db      53733 TCTTTTTTTGAGACAGGGTCTTTCTCTGTCACCCAGGCTGGAGTGCAGTGACAC-ATCAT 53675

Qy        675 AGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGT 734
              | |||||||||||||||||||||| |||||||  |||  |  | ||||||||||| |||
Db      53674 GGCTCACTGCAGCCTCAACCTCCTGGGCTCAAGCAATCCTCAAATCTCAGCCTCCCGAGT 53615

Qy        735 AGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATTTTTTTGTAGAG 794
              |||||||  |||   || ||  | |||| ||| |||||||||   ||| | ||||
Db      53614 AGCTGGGTCTATAGGCTTGAGCTACCAGGCCCGGCTAATTTTTAAATTGTTTTGTAGAGA 53555

Qy        795 ACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCT 854
              ||||||  |||| ||   ||||| |||||||||||||||||  ||||||  ||||||||
Db      53554 CAAGGGTCTCACTATGTCACCCAGGGTTGTCTTAAACTCCTGGGTTCAAGGGATCCTCCT 53495
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Qy       855 ACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATT 914
Db     53494 GCCTTGGCCTCCCAAAGTGCTAGGATTACAGGCATGAGCCACTGCACCCGGCCTGATTCC 53435

Qy       915 TCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTGCCTAT 974
Db     53434 TGATTTCTTTTTCTTTTT----------------------------------TTCTTTCT 53409

Qy       975 TTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTCA---- 1030
Db     53408 TTTTCTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGG 53349

Qy      1031 ----------GCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGC 1080
Db     53348 CACGATCTTGGCTCACTGCAAGGTCCACCTCCTGGGTTCACGCCATTCTCCTGCCTCAGC 53289

Qy      1081 CTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTT 1140
Db     53288 CTCCGGAGTAGCTGGGACTACAGGTGCCCGCCACCACACCCAGCTAAATTTTTGTATTTT 53229

Qy      1141 TAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG 1200
Db     53228 TAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTC--GTG 53171

Qy      1201 ATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGC 1260
Db     53170 ATCCGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAAGCATGAGCCACCGCGCCTGGC 53111

Qy      1261 CGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATAT 1320
Db     53110 CTTTTTCTTTTTTATTTTTTTTGAGACAGGGCTTC-CCTCTGTCACCCAGGCTGTAATGC 53052

Qy      1321 AGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCTT 1380
Db     53051 ACTGGCACTATCTTGGCTCACTGCAACCTCCACTTCCCAGGTTCAAGCAATTATCATGCC 52992

Qy      1381 TTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCA 1440
Db     52991 TCAGTCTCCTGAGTAACTGGGATTACAGGCGTGTGCCGCTACGCCCAGCTAATTTTTGTA 52932

Qy      1441 CTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAAC---CTTTATTGTTACTGTTTT 1497
Db     52931 TTTTTAGTAAAGAGGAGGTTTCCCCATGTTGGCCAAGATGGTCTCCATCTCTTGACCTCG 52872

Qy      1498 TTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTG 1557
Db     52871 TGATCTGCCCGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGCGTGAGCCACTGTGCCCG 52812

Qy      1558 CTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGAG 1617
Db     52811 GCCTGATAACAGCTTTCTATGTGCCAGCTACTGCTCCAAGTTTATATGTATTATATGTAT 52752

Qy      1618 AAATACACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACA 1677
Db     52751 TAATTCATTAGCTCATTTGTATTTATATGTACTATTAATTCCTTTTATTAGTCCATTTTC 52692

Qy      1678 AGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACAG 1737
Db     52691 ACCCTGCTGATAAAGACATACTTGAGACTGAGAAGAAAAAGATGTTTAGGCCAGGAGTGG 52632

Qy      1738 TGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTG 1797
Db     52631 TAGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGAAGGATTACCTGAGATC 52572

Qy      1798 AGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAAA 1857
Db     52571 AGGAGTTTGAGACCACCCTGGCCAACATGGCAAAACCCCATCTCTACTAAAAATACAAAA 52512

Qy      1858 ATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGA 1917
Db     52511 ATTAGTAGGGCATGGTGGTACATGCCTGTGATCTCAGCTACTTGGGAGGCTGAGGCAGGA 52452

Qy      1918 GAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCC 1977
Db     52451 GAATTGCTTGAACCTGGGAGGTGGAGGTTGTAGTGAGCCAGGATCACGCCACTGCACTCC 52392

Qy      1978 AGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATAAAGGATCG 2037
Db     52391 AGCCTGGGTGACAGAATGAGACTCCATCTAAAAAAAAAAAAAAAAAAGAAAGAAAAAGAA 52332

Qy      2038 GAGAGA 2043
Db     52331 AAAAGA 52326
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RESULT 15
AC005484/c
LOCUS       AC005484               131943 bp    DNA     linear   PRI 30-SEP-2000
DEFINITION  Homo sapiens PAC clone RP5-847O8 from 14q24.3, complete sequence.
ACCESSION   AC005484
VERSION     AC005484.2  GI:5091654
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 131943)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
   PUBMED   9847074
REFERENCE   2  (bases 1 to 131943)
  AUTHORS   Cloud,J., Wohldmann,P. and Holmes,A.
  TITLE     The sequence of Homo sapiens PAC clone RP5-847O8
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 131943)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-AUG-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 131943)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 131943)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-SEP-2000) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Jun 17, 1999 this sequence version replaced gi:3907511.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_DJ0847O8
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.
```

MAPPING INFORMATION:
This clone from chromosome 14 was provided by Dr. Pieter de Jong, Roswell Park Cancer Institute, Human Genetics Department, Elm and Carlton Streets, Buffalo NY 14263-0001 USA.

SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.
The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP5-892G5; the clone sequenced to the right is RP4-592G7, 200 bp overlap. Actual start of this clone is at base position 1 of RP5-847O8; actual end is at base position 131747 of RP5-847O8.

FEATURES	Location/Qualifiers
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	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="14"
	/map="14q24.3"
	/clone="RP5-847O8"
	/clone_lib="RPCI-5"
repeat_region	1058. .1098
	/rpt_family="AT_rich"
repeat_region	1762. .2225
	/rpt_family="MaLR"
repeat_region	2305. .2587
	/rpt_family="Alu"
repeat_region	2937. .3086
	/rpt_family="L2"
repeat_region	3293. .3591
	/rpt_family="Alu"
repeat_region	3651. .3916
	/rpt_family="L1"
repeat_region	3917. .3943
	/rpt_family="(TA)n"
repeat_region	4815. .4841
	/rpt_family="AT_rich"
repeat_region	5153. .5244
	/rpt_family="L1"
repeat_region	5728. .6008
	/rpt_family="Alu"
repeat_region	6009. .6034
	/rpt_family="(CAA)n"
misc_feature	8080. .8468
	/note="match to EST R05271 (NID:g755891) ye91b03.s1"
STS	8080. .8277
repeat_region	8284. .8589
	/rpt_family="Alu"
misc_feature	8649. .9039
	/note="match to EST R05328 (NID:g755948) ye91b03.r1"
repeat_region	8857. .9007
	/rpt_family="MIR"
repeat_region	9062. .9152
	/rpt_family="MIR"
repeat_region	9216. .9288
	/rpt_family="MIR"
repeat_region	9476. .9770
	/rpt_family="Alu"
STS	9711. .10034
repeat_region	10004. .10114
	/rpt_family="Alu"
repeat_region	10115. .10135
	/rpt_family="(TAAA)n"
repeat_region	10136. .10158
	/rpt_family="Alu"
repeat_region	10205. .10501
	/rpt_family="Alu"
repeat_region	10513. .10819
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repeat_region	10890. .11242
	/rpt_family="MaLR"
repeat_region	11246. .11519
	/rpt_family="Alu"
repeat_region	11567. .11996
	/rpt_family="L2"
repeat_region	12006. .12113
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repeat_region	12123. .12146
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repeat_region	12147. .12430
	/rpt_family="Alu"
repeat_region	12445. .12535
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repeat_region	12527. .13097
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repeat_region	13217. .13339
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repeat_region	13389. .13994
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repeat_region	14138. .14158
	/rpt_family="AT_rich"
repeat_region	14195. .15071
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repeat_region	15048. .15521
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repeat_region	15520. .15992
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repeat_region	16257. .16556
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repeat_region	16569. .16963
	/rpt_family="L1"
repeat_region	17016. .17039
	/rpt_family="AT_rich"
repeat_region	17073. .17182
	/rpt_family="MIR"
repeat_region	17252. .17452
	/rpt_family="MaLR"
repeat_region	17473. .17991
	/rpt_family="L2"
repeat_region	18106. .18192
	/rpt_family="MER1_type"
repeat_region	18193. .18504
	/rpt_family="Alu"
repeat_region	18505. .18588
	/rpt_family="MER1_type"
repeat_region	18624. .18904
	/rpt_family="L1"
repeat_region	19144. .19368
	/rpt_family="Alu"
repeat_region	20030. .20159
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repeat_region	20167. .20317
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	/rpt_family="Alu"
repeat_region	20618. .20753
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repeat_region	20802. .20954
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repeat_region	20955. .21256
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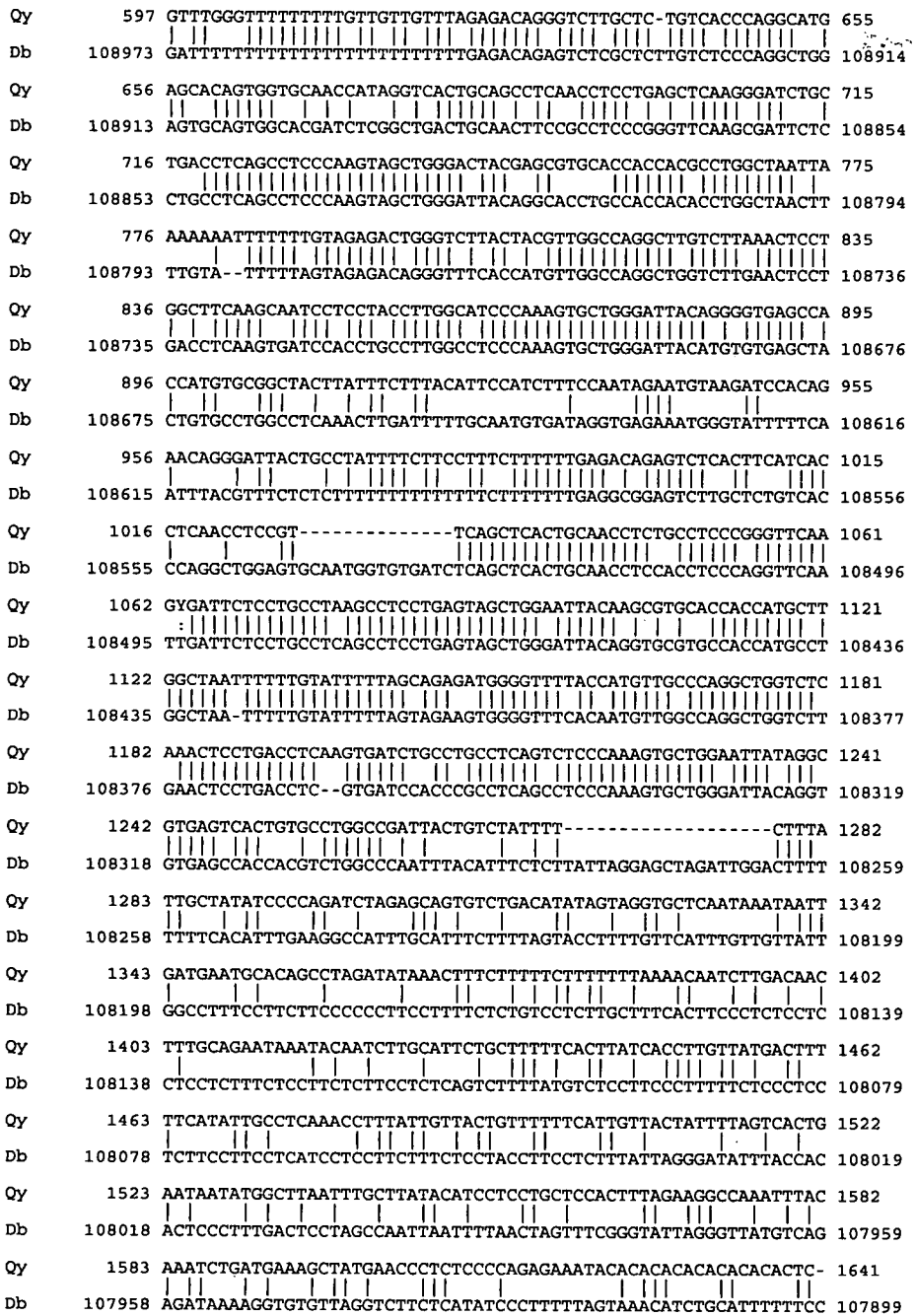
Query Match 17.9%; Score 447.8; DB 8; Length 131943;
Best Local Similarity 61.3%; Pred. No. 1.3e-80;
Matches 913; Conservative 1; Mismatches 523; Indels 52; Gaps 10;



Search completed: February 17, 2006, 13:51:33
Job time : 12648 secs

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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 10:20:55 ; Search time 9872 Seconds
(without alignments)
11853.170 Million cell updates/sec

Title: US-10-607-806-1-C7256_COPY_7000_9500
Perfect score: 2499
Sequence: 1 gtcgtgtcactgctgtccag.....tttgagaccagcctggacaa 2501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	505.4	20.2	507	5	BU785040	BU785040 in43g09.x
	2	344.2	13.8	4087	4	BC024593	BC024593 Homo sapi
	3	341	13.6	3990	4	HSM803026	AL713681 Homo sapi
c	4	337.2	13.5	15970	9	AQ839852	AQ839852 260L13-C5
c	5	315.8	12.6	897	6	CD557847	CD557847 AGENCOURT
	6	311	12.4	3095	4	CR858326	CR858326 Pongo pyg
c	7	307.2	12.3	5797	4	CR749233	CR749233 Homo sapi
c	8	301.2	12.1	1605	4	CR860521	CR860521 Pongo pyg
	9	301.2	12.1	1863	4	CR599842	CR599842 full-leng
	10	300.6	12.0	946	5	BQ958903	BQ958903 AGENCOURT
c	11	298	11.9	918	5	BQ706343	BQ706343 AGENCOURT
	12	293.6	11.7	736	8	CX780936	CX780936 HESC3_2_B
	13	290.6	11.6	3092	4	CR613629	CR613629 full-leng
c	14	288.2	11.5	855	5	BQ681302	BQ681302 AGENCOURT
c	15	287.6	11.5	769	5	BQ710315	BQ710315 AGENCOURT
c	16	285.2	11.4	4088	4	HSM808459	BX648311 Homo sapi
	17	283	11.3	3165	4	CR859576	CR859576 Pongo pyg
c	18	281.6	11.3	800	1	AU120942	AU120942 AU120942
	19	281.4	11.3	3259	4	CR860168	CR860168 Pongo pyg
	20	280.4	11.2	672	6	CA431692	CA431692 UI-H-DF0-
	21	280	11.2	3474	4	HSM800886	AL110229 Homo sapi
	22	278.8	11.2	658	9	AQ393450	AQ393450 CITBI-E1-
c	23	277.6	11.1	877	9	AQ739838	AQ739838 HS_5505_A
	24	277.2	11.1	1875	4	BC009270	BC009270 Homo sapi
c	25	276.6	11.1	3990	4	HSM803026	AL713681 Homo sapi
	26	276.4	11.1	4828	4	HSM802759	AL390128 Homo sapi
c	27	276.2	11.1	881	5	BU521286	BU521286 AGENCOURT
	28	274.8	11.0	3552	4	CR860263	CR860263 Pongo pyg
	29	273.8	11.0	736	6	CA427039	CA427039 UI-H-DF0-
c	30	273.4	10.9	629	5	BX509360	BX509360 DKFZp686J
c	31	273.4	10.9	2230	4	CR859082	CR859082 Pongo pyg
	32	272.4	10.9	652	6	CA427045	CA427045 UI-H-DF0-
	33	272.4	10.9	666	6	CA431783	CA431783 UI-H-DF0-
c	34	272.4	10.9	815	8	CX785622	CX785622 HESC3_49_
c	35	272.2	10.9	922	5	BU501973	BU501973 AGENCOURT
c	36	272	10.9	617	3	BI861844	BI861844 603388872
	37	271.8	10.9	644	7	CN480313	CN480313 UI-H-EU0-
	38	271.6	10.9	1042	5	BX377759	BX377759 BX377759
	39	271.6	10.9	2097	4	CR614786	CR614786 full-leng
c	40	271.4	10.9	603	1	AL707313	AL707313 DKFZp686P
c	41	271.2	10.9	5325	4	HSM804049	AL832738 Homo sapi
c	42	271.2	10.9	5785	4	HSM802309	AL137734 Homo sapi
c	43	270.6	10.8	2330	4	CR615928	CR615928 full-leng
	44	270.4	10.8	618	9	BZ609884	BZ609884 WHACH76TF
	45	270	10.8	665	5	BU633001	BU633001 UI-H-DF0-

ALIGNMENTS

RESULT 1
BU785040/c
LOCUS BU785040 507 bp mRNA linear EST 11-OCT-2002
DEFINITION in43g09.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6125008 3', mRNA sequence.
ACCESSION BU785040
VERSION BU785040.1 GI:23830576
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 507)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 443.
FEATURES Location/Qualifiers
source 1. .507
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6125008"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 20.2%; Score 505.4; DB 5; Length 507;
Best Local Similarity 99.8%; Pred. No. 2.3e-35;
Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1506 TACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTT 1565
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Db        507 TACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTT 448

Qy       1566 TAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGAGAAATACAC 1625
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Db        447 TAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGAGAAATACAC 388

Qy       1626 ACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCT 1685
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Db        387 ACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCT 328

Qy       1686 GCATTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGACTCAA 1745
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Db        327 GCATTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGACTCAA 268

Qy       1746 GCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTC 1805
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Db        267 GCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTC 208

Qy       1806 GAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAAAATTAGCTG 1865
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Db        207 GAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAAAATTAGCTG 148

Qy       1866 GGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCT 1925
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        147 GGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCT 88

Qy       1926 TGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGG 1985
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          87 TGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGG 28

Qy       1986 CGACACAGCGAGACTCTATCTCAAAAA 2012
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Db          27 CGACACAGCGAGACTCTATCTCAAAAA 1
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RESULT 2
BC024593
LOCUS BC024593 4087 bp mRNA linear HTC 29-JUN-2004
DEFINITION Homo sapiens cDNA clone IMAGE:3914314, with apparent retained intron.
ACCESSION BC024593
VERSION BC024593.1 GI:22137609
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4087)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 4087)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 22 Row: m Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
This clone has the following problem: retained intron.

FEATURES Location/Qualifiers
source 1. .4087
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3914314"
/tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 13.8%; Score 344.2; DB 4; Length 4087;
Best Local Similarity 58.3%; Pred. No. 6.6e-22;
Matches 859; Conservative 1; Mismatches 544; Indels 69; Gaps 12;

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Qy        599 TTGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGC 658
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Db       2019 TTTGAAATTTGTTTGTTTGTGTTTTGAGACAGGGTCTGGGTCTGCCACCCAGGCTGGAGT 2078

Qy        659 ACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGA 718
              |||||||  | ||||| ||| ||||||| |||||| | | || |||| |||   || |
Db       2079 GTAGTGGTGTGATCATAGCTCAATGCAGCCCCAACCTTCCGGGCGCAAGTGATGCTCTCA 2138

Qy        719 CCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAA 778
              ||||||||||  |||||||||||||||  || ||  ||||||| ||   |||||  | |
Db       2139 CCTCAGCCTCCTGAGTAGCTGGGACTACAGGCATGTGCCACCACACCCTCCTAATATATA 2198

Qy        779 AAAT-----TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTC 833
                  |     |||||||||||||   ||| | | || |||| |||| || ||||  |||||
Db       2199 TTTTTTTTATTTTTTGTAGAGATGAGGTTTCATTATGTTGCCCAGACTGGTCTGGAACTC 2258
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Qy       834 CTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGC 893
Db      2259 CTGGC-TCAAGTGATCCTCCCTCCTTGCCCTCCCGAAGTGTTGGGATTGCGTGCACGAGC 2317

Qy       894 CACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCAC 953
Db      2318 CACCACATCTGGCCTGTTTGATTATTTAATTTTTTTTT---------------------- 2356

Qy       954 AGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTGAGACAGAGTCTCACTTCATC 1013
Db      2357 --------------TTTTTTTTTTGAGATAGAGTCTCGCTCTGTCGCTCAGGCTGGAGT 2402

Qy      1014 ACCTCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTG 1073
Db      2403 GCAGTGGTGTGATCTCGGCTCGCTGCAACCCCCGTCTCCCGGGTTCAGGTGATTTTCCTG 2462

Qy      1074 CCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTT 1133
Db      2463 TGTCAGCCTCCCGAGTAGCTGGGGTTACAGGTGTCCACCACCAAGCCTGGCTAA-TTTTT 2521

Qy      1134 GTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACC 1193
Db      2522 GTATTTTTAGTACAGCTGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACC 2581

Qy      1194 TCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGT 1253
Db      2582 TC--GTGATCTGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGT 2639

Qy      1254 GCCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCT-AGAGCAGTGTC 1312
Db      2640 GCCCAGCCGATTATTTAATATTTTTATTTGCTTCCTCTTTGCAGAAATGATTTGATTGCT 2699

Qy      1313 TGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGA----TATAAAC 1368
Db      2700 AGGCTTATATTCAGCCATCATTAACCAAATGTGCTGAGCCCTGACTCAGGGCTTTTACAT 2759

Qy      1369 TTTCTTTTTCTTTTTTTAAAACAATCTTGACAACTTTGCAGAATAAAT------------ 1416
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Qy      1417 ACAATCTTGCATTCTGCTTTTTCACTTATCACCTTGTTATGACTTTTTCATATTGCCTCA 1476
Db      2820 ATAATAGTAAGACAAAACTTTTAGATTTTATTGCCAATATGAGTTAGGAAAACAGTCCAG 2879

Qy      1477 AACCTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTA 1536
Db      2880 AGAATTTCTGTATATAATAATTGTATTTCTGTGGGTTTTTTTTGTAGGTTCAATTATTTT 2939

Qy      1537 ATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAG 1596
Db      2940 AGCTGGGCACAATCATCCTTCTGCCAGGGTGTATGGGTCATTTT---TTTTTCAAGAGGG 2996

Qy      1597 CTATGAACCCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGTTTTTTT 1656
Db      2997 AATTATTATTTTTGGTTACAAAAGTAATTGTATTGTGGTATCTATAAAGAATACTTCAAA 3056

Qy      1657 TTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAA 1716
Db      3057 CTGAAGAGTTTTAAAATGTGTAGAATACAGAATCTGAGCTTCAGTCTACTGGCAAGATGC 3116

Qy      1717 AAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAG 1776
Db      3117 AATTTAGGCC---GGGTGCAGTGACTCACGCCTGCAGTCTTAGCCCTTTGGGAGGCCGA- 3172

Qy      1777 GTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCT 1836
Db      3173 GTGGGAGGATTGCTTGAGCTCAAGAGTTTGAGACAGGGCTGAGCAATGTAGTGGGACCTC 3232

Qy      1837 ATCTCTACT-AAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGC 1895
Db      3233 GTCTCTATAAAAAAATTTAAAGGTTAGCCTGGTGTGGTGGTGTGCGCCTGTGGTCCTGGC 3292

Qy      1896 TACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGC 1955
Db      3293 TACTTGGGAGGCTGTGATGGGAGGATCGCTGGAGCGTGGGAGGTCAAGGCTGCGGTGGGT 3352

Qy      1956 CGAGATCCCACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAAT 2015
Db      3353 CATGGTTGTGCCACTGCACTTCAGCCTGGGTGACAGAGTAAGACCCTGTCTAAAAAGCAA 3412

Qy      2016 AAATAAATAAAATAAAGGATCGGAGAGAAACAA 2048
Db      3413 AATAAGATGCAGTTTGGAGTGTAAAATAGAGAA 3445
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RESULT 3
HSM803026
LOCUS       HSM803026              3990 bp    mRNA    linear   HTC 16-APR-2005
DEFINITION  Homo sapiens mRNA; cDNA DKFZp761O0217 (from clone DKFZp761O0217).
ACCESSION   AL713681
VERSION     AL713681.1  GI:19584382
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3990)
  AUTHORS   Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp761O0217) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp761O0217
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .3990
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="RZPD:DKFZp761O0217"
                     /db_xref="taxon:9606"
                     /clone="DKFZp761O0217"
                     /tissue_type="amygdala"
                     /clone_lib="761 (synonym: hamy2). Vector pSport1; host
                     DH10B; sites NotI + SalI"
                     /dev_stage="adult"
                     /note="cytochrome c"
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     CDS             61. .378
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                     TNE"
ORIGIN
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Query Match            13.6%;  Score 341;  DB 4;  Length 3990;
Best Local Similarity  57.5%;  Pred. No. 1.3e-21;
Matches  856;  Conservative    1;  Mismatches  541;  Indels   91;  Gaps   10;

Qy        604 TTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGT 663
Db       2522 TTTTCTCATTTATTTTTTCTGAGACGGAGTTTCGCCCTTTTCGCCCAGGCTGAGTACAGT 2581

Qy        664 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 723
Db       2582 GGTGCAATC-----TCACTGCAACCTCCGCCTTCCAGTTGCAAGTGATTCTCCTGCCTCA 2636

Qy        724 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATT 783
Db       2637 GCCTCCTGAGTAGCTGGGATTGCAGGCACCCGCCACCACGCCTGGCTAATTTTTGTA--T 2694

Qy        784 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAA 843
Db       2695 TTTAGTGGAGATGGTGTTTCACCATGTTGGCCAGACTGGTCTTGGACTCCTGACCTC-- 2752

Qy        844 GCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 903
Db       2753 GTGATCCACCCACCTTGGCCTCCCAAAGTTCTAGGATTACAGGTGTGAGCCACCACGTCC 2812

Qy        904 GGCTACTTATT----------------------------------------------- 914
Db       2813 GGCCAATTTTTCTCATTTCTATGCCTCCTATATTAAGGTCTGTGTTGGCACAGATGAGTA 2872

Qy        915 ------TCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACT 968
Db       2873 ACTGCCATGTTCTAGGTCAGTTATACCCAAGCACTTCTGGTGGTTTAAAATGTGATTCTG 2932

Qy        969 GCCTATTTTCTTCCTTTCTTTTTGAGACAGAGTCTCACTTCATCACC----------- 1016
Db       2933 TAACTTTTTTATTTTTATTTTTTGAGATAATTTCACTCTTGTTGCCCAGGCTGGAGTGC 2992

Qy       1017 -TCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCC 1075
Db       2993 AATGGCGTGATCGCTGCTCACCGCAACCTCCGCCTTCCAGGTTCAAGCGATTCTCCTGAC 3052

Qy       1076 TAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGT 1135
Db       3053 TCAGCCTCTCAAGTAGCTGGGATTACAAGCATGCGCCACCATGCCCAGCTTATTT--TGT 3110

Qy       1136 ATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTC 1195
Db       3111 GTTTTTAGTAGAGACAGGGTTTCTCCATGCTGGACAGGCTGGTCTTGAACTCCCGACGTC 3170

Qy       1196 AAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGC 1255
Db       3171 GGGTGATCTGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGC 3230

Qy       1256 CTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGA 1315
Db       3231 CTGGCCAATTA---TGTAATTTTTTAAAAAGGACATTTCTATCAGGGATATATACCTTCA 3287

Qy       1316 CATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTT 1375
Db       3288 GAAATAAGGAAATAGGGGAAAAAAAGAGCACTATAAACCACATGTTTTCATTTCTAGTGC 3347

Qy       1376 TTCTTTTTTTAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTT 1435
Db       3348 TTCGCTGTAAGTGGCTAGGTTGGTAGAATCAAAAACAAGGGCCAGATGTATTTAAGGGGT 3407

Qy       1436 TTTCACTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAACCTTATTGTTACTGTT 1495
Db       3408 ATTCAGATGCCACCTACATGCTTATTTTGTCTAGAACAGTGCTGTCTAATAGAACTTTCT 3467

Qy       1496 TTTTCATTGTTACTATTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCC 1555
Db       3468 GTGACGATGGATATTTTGTAGACTTT------TGCTGTCCAGTGTGGTAGCCACTAACCA 3521

Qy       1556 TGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAG 1615
Db       3522 CATGTGGCTGTTAAGCCCTTGAAATATAGCTAGTGTGACTAGAAAGTATTTTATTTTAAA 3581

Qy       1616 AGAAATACACACACACACACACACTCACACACAGTTTTTTTTAATGTTTGCAACTAAGA 1675
Db       3582 TTTACATAGGCACAAGTGGCTAGTGGCTACTGTATTGACATTCTGGGTCTAGGACTAGAA 3641

Qy       1676 CAAGAAACCTGCATTAGAGG--ATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGC 1733
Db       3642 CCAGTGGTCTGTAACAAAAGTACTTTCTCTTTACTCTATTAAATCTAGAATTAGCCGGGC 3701

Qy       1734 ACAGTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGA 1793
Db       3702 ATGGTCGCTCATGCCTGTGGTCCCAGCACTTTGGGAGGCCAAGGCAGGCAGATCACTTGA 3761

Qy       1794 GGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATAC 1853
Db       3762 GGTCGGGCGTTTGAGACCAGCCTGGTCAACATGGCGAAACCCTGTCTCTACAAAAAACAT 3821

Qy       1854 AAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC 1913
Db       3822 AAAAGTTAGCCAGGTGTGGTGGTGGGCACCTGTAGTCTCAGCTACTTGGGAGGCTGAGGC 3881

Qy       1914 AAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCA 1973
Db       3882 ACAAGAATCACTTGAACTTGGGAGGTGGAGGTTGCAGTGAGCCAGGATTGTGCCACTGCA 3941

Qy       1974 CTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAA 2022
Db       3942 CTCAAGCCTGGGTGAC-GAGTGAAACTGTCTCCAAAAAAAAAAAAAAAA 3989
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RESULT 4
AQ839852/c
LOCUS       AQ839852                15970 bp    DNA     linear   GSS 31-MAR-2000
DEFINITION  260L13-C56 CITB Homo sapiens genomic clone 260L13, genomic survey
            sequence.
ACCESSION   AQ839852
VERSION     AQ839852.1  GI:6652484
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 15970)
  AUTHORS   Carpten,J.D., Makalowska,I., Robbins,C.M., Scott,N., Sood,R.,
            Connors,T.D., Bonner,T.I., Smith,J.R., Faruque,M.U., Stephan,D.A.,
            Pinkett,H., Morgenbesser,S.D., Su,K., Graham,C., Gregory,S.G.,
            Williams,H., McDonald,L., Baxevanis,A.D., Klingler,K.W. and
            Landes,G.M.
  TITLE     A 6-Mb high-resolution physical and transcription map encompassing
            the hereditary prostate cancer 1 (HPC1) region
  JOURNAL   Genomics 64 (1), 1-14 (2000)
   PUBMED   10708513
COMMENT     Contact: Carpten JD
            Cancer Genetics Branch
            National Human Genome Research Institute/National Institutes of
            Health
            Bldg. 36, Room 3D04, 36 Convent Drive, Bethesda, MD
            Tel: 301 435 5626
            Fax: 301 435 5465
            Email: jdc@nhgri.nih.gov
            Class: shotgun.
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match             13.5%;  Score 337.2;  DB 9;  Length 15970;
Best Local Similarity   57.8%;  Pred. No. 1.1e-21;
Matches  905;  Conservative    1;  Mismatches  529;  Indels  131;  Gaps   12;

Qy        598 TTTGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAG 657
Db       6787 TTTTTATTTTTATTTATTTTTTTTTGAGGTGGAGTATCGCTATGTCACCCAGGCTGGAG 6728

Qy        658 CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTG 717
Db       6727 TGCAGTGGCATGATATCAGCTCACTGCAACCTTCACCTGCTAGATTCAAGCAGTTCTCGT 6668

Qy        718 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAA 777
Db       6667 GACTCAGCCTCCTGAGTAGCTGTGATTACAGGCACATGCCACCATGCTCAGCTAACT-TT 6609

Qy        778 AAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGG 837
Db       6608 TGTATTTTTAGTAGAGACAGGGTCTCACCATGTTGGCCAGGCTGGTCTGGAACTCCTGA 6549

Qy        838 CTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACC 897
Db       6548 CCTCAAGTGATCCGCCCTCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACT 6489

Qy        898 ATGTGCGGCTACTTATTTCTTT--------ACATTCCATCTTTCCAATAGAATGTAAGAT 949
Db       6488 GCGCCCAGCCTCTGAGTTCTTTTAAGTCAGAAACTTGAGCTCTTCAGCTCTGATAAATTT 6429

Qy        950 CCACAGAACAGGGATTACTGCCT--ATTTCTTCCTTTCTTTTTTGAGACAGAGTCTCAC 1007
Db       6428 GGGGGGCAAGGGGACTAATTTTTCTTTTTCTTTTCTTTTTTTTAAGATGGAGTCTTGC 6369

Qy       1008 TTCATCACCTCAACCTCCGTTCA--------------GCTCACTGCAACCTCTGCCTCCC 1053
Db       6368 TGTGTTGCCCAGGGTGGAGTGCAGTGGTGTGATCTTGGCTCACTGCAACCTCTGCCTCCC 6309

Qy       1054 GGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCA 1113
Db       6308 AGGTTCAAGCAATTCTCCTGCCTCAGCTTACTGAGTAGCTGGGACTGCAGGCCTGTGCCA 6249

Qy       1114 CCATGCTTGGCTAATTTTTTGTATTTTTAGCAGAGATGGGGTTTACCATGTTGCCCAGG 1173
Db       6248 CCACTCTCAGCTAA-TTTTTGTATTTTTAGTAGAGACAGGGTTTCAGCACATTGGCCAGG 6190

Qy       1174 CTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAA 1233
Db       6189 CTGGTCTCGATCTCCTGACCTCAAGTGATCTGCCTACCTCGTCTCCCCAAAGTGCTGGGA 6130

Qy       1234 TTATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCC 1293
Db       6129 TTACAGGCAAGAGCCACCACACCTGGCCCTT---GGGGGATGTTATTTCTTTGACAAGTT 6073

Qy       1294 CCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCAC 1353
Db       6072 TTGCCTTTCAAATTATATCTGTTGTCTCTTTCAGGAACTCTGTTTAGTTATATTTTGGGT 6013

Qy       1354 AGCCTAGATATAAACTTTCTTTTTCTTTTTTAAAACAATCTTGACAACTTTGCAGAATA 1413
Db       6012 CTTCTAGATTAATCCTTTAATTTTTTAAAATATCTATACGGTTCATCTCTTTGGCAATTA 5953

Qy       1414 AATACAATCTTGCATTCTGCTTTTTCACTTATCACCTTGTTATGACTTTTTCATATTGCC 1473
Db       5952 GTTCTACTTTATACTTTTTCCTTAATTTTTATTTTCCAACTCTTATTTAAATTTCTGTCA 5893

Qy       1474 TCAAACCTTTATT-----------GTTACTGTTTTTTCATTGTTACTATTTTAGTC---- 1518
Db       5892 TATTTTGTTCATTTCTAAGAGTTATTTCATATTTTTTCACTGTTCCTTTTTTTTTCTTTA 5833

Qy       1519 ---------ACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGA 1569
Db       5832 GGCTAGTCAAGTGATTATTGTTCCTTTTTTAATAGTGTCATATTGTTTCAGGGATACAAA 5773

Qy       1570 A-------------------------------GGCCAAATTTACAAATCTGATGAAAGC 1597
Db       5772 ATCTCTTACCTTTCTAAGAATTGATTATACTTGGGTATATTTTATATTTAGGGGAGAATA 5713

Qy       1598 TATGAACCCTCTCCCCAGAGAAATACACACACACACACACACTCACACACAGTTTTTTTT 1657
Db       5712 GGGGTTTTTTGTTTGTTTTGTATTGTTGCTGTTGTTTTGTTGTTCAGTTCTCCTGTTTTT 5653

Qy       1658 TAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAAA 1717
Db       5652 TAACTTTTTCTGTTTTGTAATTTTGTTCTCTGTCTGTCATGGTAGTTCTCAAATGTTTTG 5593

Qy       1718 AATAACTCAGTTGGGCACAGTGACTCA-------------------------------- 1744
Db       5592 TGGTCTTCGGTTGTCCACAGTGAAAAATTGTTTTAAAGCACTTGGGGCAGAGCTTATAAA 5533

Qy       1745 ----------AGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAG 1794
Db       5532 CCAACGGATTTGGCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCA--TGAG 5475

Qy       1795 GTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATAC- 1853
Db       5474 GTCAGGAGATCGAGACCATCCTGGCTAACACAGTGAAACCCTGTCTCTACTAAAAATACA 5415

Qy       1854 AAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC 1913
Db       5414 AAAAATTAGCCGGGCGTGGTGGCGGGCACCAATAGTCCCAGCTACTCGGGAGGCTGAGGC 5355

Qy       1914 AAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCA 1973
Db       5354 AGGAGAATGGCGTGAACCTGGGAGGCGGAGCTTGCAGTGAGCCAAGATCGCACCACTGCA 5295

Qy       1974 CTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAATAAAGG 2033
Db       5294 CTTGAGCCTAGGCAACAAAGCGAGACTGTCTCAAAAAAAAAATAAAAATAAAAATAAACC 5235

Qy       2034 ATCGGA 2039
Db       5234 AATGGA 5229

RESULT 5
CD557847/c
LOCUS       CD557847                 897 bp    mRNA    linear   EST 11-JUN-2003
DEFINITION  AGENCOURT_14423258 NIH_MGC_180 Homo sapiens cDNA clone
            IMAGE:30390116 5', mRNA sequence.
ACCESSION   CD557847
VERSION     CD557847.1  GI:31583915
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 897)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM464  row: k  column: 21
            High quality sequence stop: 636.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_180"
                     /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site_1: NotI;
                     Site_2: EcoRV (destroyed); Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.68 kb. Library was
                     constructed by (Invitrogen). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             12.6%;  Score 315.8;  DB 6;  Length 897;
  Best Local Similarity   68.1%;  Pred. No. 5.1e-19;
  Matches  469;  Conservative    1;  Mismatches  213;  Indels    6;  Gaps    2;

Qy        583 TGTAAGTGGTGACAGTTTGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTG 642
              |||| |       |  ||   || |||| | ||  | ||| |||||| |||||  |||||
Db        765 TGTATGCATCCCGATATTATTTTATTTTATTTTTATTTTTTGAGACATGGTCTCACTCTG 706

Qy        643 TCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGC 702
              |  ||||| |  |||  ||||||    | |  || |||||||| |||| ||||||   |
Db        705 TTGCCCAGCCTGGAGTGCAGTGGCAGGATCTCAGCTCACTGCAACCTCCACCTCCCAGGT 646

Qy        703 TCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCAC 762
              |||||  ||   |  |||||||||||||||||||||||||| |||  | ||||||||||||
Db        645 TCAAGCAATTCTCCCACCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGCACCACCAC 586

Qy        763 GCCTGGCTAATTAAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTT 822
              |||  |||||||         ||||  ||| |||  |||| || | | | ||||||||||
Db        585 GCCCAGCTAATTTTTTTGTATTTTAAGTACAGATGGGGTTTTGCCATGCTGGCCAGGCTC 526

Qy        823 GTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTA 882
              ||| ||| ||||| | |||||  |||  || |||||||| ||||||||||||||||||||
Db        525 CTCTCAAATTCCTGACCTCAAGTGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTA 466

Qy        883 CAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAAT 942
              |||| |||||||||| ||  | ||| | |  |  | |  | | | |       | | || |
Db        465 CAGGCGTGAGCCACCGTGCCCAGCTGCATCCTGATATTTAATGCTTGCCAGAATTTGATT 406

Qy        943 GTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGT 1002
              | |  || |  |           |  |   | |||| ||    |      | | |     |
Db        405 GCACCATGCTTATTGGCTTCTATCTTTTTTTTTTTTTTTGAGATGGAGACTCACTCTCTCT 346

Qy       1003 CTCACTTCATCACCTCAACCTCCGT----TCAGCTCACTGCAACCTCTGCCTCCCGGGTT 1058
              ||| |    |    | |      ||    |||||||||||||||||  | ||| |||||
Db        345 CTCCCAGGCTGGAGTGCAGTGGTGTGATCTCAGCTCACTGCAACCTCCACTTCCTGGGTT 286

Qy       1059 CAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATG 1118
              ||||:|||||||||| || ||||||| |||||||||| | ||||   |||  ||||||
Db        285 CAAGCGATTCTCCTGTCTCAGCCTCCAGAGTAGCTGGGACTACAGATGTGTGCCACCACA 226

Qy       1119 CTTGGCTAATTTTTTGTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGT 1178
              | |||||||  ||| |||||||||| |||||||||||||| |||||||| |||| ||  |
Db        225 CCTGGCTAA--TTTCGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGACTAAT 168

Qy       1179 CTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATA 1238
              ||| |||||||||||||| ||||||  ||||||||   | ||||||||||| |||  ||| |
Db        167 CTCGAACTCCTGACCTCAGGTGATCCGCCTGCCTTGGCCTCCCAAAGTGTTGGGGTTACA 108

Qy       1239 GGCGTGAGTCACTGTGCCTGGCCGATTAC 1267
              ||||||||| |||    || | | | || |
Db        107 GGCGTGAGCCACCACCCCAGCCGGCTTCC 79


RESULT 6
CR858326
LOCUS       CR858326               3095 bp    mRNA    linear   HTC 12-NOV-2004
DEFINITION  Pongo pygmaeus mRNA;. cDNA DKFZp469P012 (from clone DKFZp469P012).
ACCESSION   CR858326
VERSION     CR858326.1  GI:55727613
KEYWORDS    HTC.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1  (bases 1 to 3095)
  AUTHORS   Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,
            Osanger,A., Fobo,G., Han,M. and Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp469P012) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469P012
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
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                     DH10B; sites SfilA + SfilB"
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ORIGIN

  Query Match             12.4%;  Score 311;  DB 4;  Length 3095;
  Best Local Similarity   56.6%;  Pred. No. 6.1e-19;
  Matches  883;  Conservative    1;  Mismatches  511;  Indels  166;  Gaps   10;

Qy         584 GTAAGTGGTGACAGTTTGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGT 643
               || ||      ||    | | ||||||  |||  | |  |||  ||||  | ||||  || |||
Db        1570 GTGAGCCACTACCTGTAGCGTTTTTGTTTTGTTTGTTTTTGAGATGGAGTCTCACTTTGT 1629

Qy         644 CACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCT 703
                 ||||  |  |||  |||||||| | |  || ||||||||||||  |||||    | |
Db        1630 TGCCCAACCTGGAGTGCAGTGGTGCGATCTCAGCTCACTGCAGCCTCCGCCTCCCAGGTT 1689

Qy         704 CAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACG 763
               ||||  ||   |  ||||||||||||||||||||||||||||  || ||  |||||||
Db        1690 CAAGCAATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTAGAGGCTTGTGCCACCACA 1749

Qy         764 CCTGGCTAATTAAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTG 823
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Db        1750 CCCAGCTAATT---TTTTGTATTTTATGGAGACAGGGTTTCACCATGTTGCCCAGGCTGG 1806

Qy         824 TCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTAC 883
               ||||| |||||||   ||| ||| ||| || ||||  || ||||||  ||||| |||||||
Db        1807 TCTTAGACTCCTGAGCTCAGGCACTCCGCCCACCTCAGCCTCCCAAGGTGCTAGGATTAC 1866

Qy         884 AGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTC---------------------- 925
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Qy        939 GAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACA 998
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Qy       1044 TCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAA 1103
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Qy       1104 GCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTTTAGCAGAGATGGGGTTTTACCAT 1163
Db       2167 GCTCCTGCCACCATGCCTGGCTAA-TTTTTGTATTTTTAGTGGAGACAAGGTTTCATCAT 2225
Qy       1164 GTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAA 1223
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Qy       1224 AGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCC-GATTACTGTCTATTTTCTTTA 1282
Db       2286 GTTGCTGGGATTACATGCGTGAGCCACCACACCCGGCCTGCTTAACATATATCTTGACCA 2345
Qy       1283 TTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATT 1342
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Qy       1343 GATGAATGCACAGCCTAGATATAAACTTTCTTTTTCTTTTTTTAAAACAATCTTGACAAC 1402
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Qy       1403 TTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCACTTATCACCTTGTTATGACTTT 1462
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Qy       1643 CACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTG 1702
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Qy       1883 CTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGA 1942
Db       2865 CTGTAATCCCAGCCTCTTAGGCAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGA 2924
Qy       1943 GGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCT 2002
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Qy       2003 ATCTCAAAAAAATAAATAAATAAAATAAAGGATCGGAGAGAAACAAAACTAATAAGATTC 2062
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Qy       2063 C 2063
Db       3045 C 3045
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LOCUS       CR749233               5797 bp    mRNA    linear   HTC 19-AUG-2004
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686C0331 (from clone DKFZp686C0331).
ACCESSION   CR749233
VERSION     CR749233.1  GI:51476197
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 5797)
  AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project. This clone (DKFZp686C0331) is available at
            the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
            Berlin, Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686C0331
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
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     CDS             103. .1725
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                     IIHTEKKPYKCEECGKAFNRSSTLTTHKIIHTGEKPYKCEECDKAFKYSYTLTTHKRI
                     HTEDKPYKCEECGKAFKYSSTLTTHKRIHTGEKPYKCEECGKAFKRSSDLTTHKIIHT
                     GEKPYKCEECGKAFKYSSNLTTHKKIHTGERPYKCEECGKAFNQSSILTTHKRIHTGE
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ORIGIN

Query Match 12.3%; Score 307.2; DB 4; Length 5797;
Best Local Similarity 56.9%; Pred. No. 8.8e-19;
Matches 902; Conservative 1; Mismatches 569; Indels 114; Gaps 14;

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Qy        665 GTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAG 724
Db       4916 GCACGATCTCGGCTCACTGCAACCTCTGCCTCCTGGGTTACACCATTCTCCCG-CCTCAG 4858

Qy        725 CCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATTT 784
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Qy        785 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAG 844
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Qy        845 CAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCG 904
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Qy       1025 CGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCC 1084
Db       4619 --CTCAGCACACTGAAACCTCCACCTCCCAGGTTCAAGCCATTCTCCTGCCTCGGCTTCC 4562

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Db       4450 GCCCGACGTCACCTACCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGTCCAGCCCA- 4392

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Qy       1385 TAAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCACTTA 1444
Db       4278 TGGAATAGAAAGGATAAATGCTAGAGGTGATAGATACCTTATTTACCCTAATGTAATTAC 4219

Qy       1445 TCACCTTGTTATGACTTTTTCATATTG-----CCTCAAACCTTTATTGTTACTGTTTTTT 1499
Db       4218 TACATATTGTATGCCTGAATCAAAATATTCTCTATAAGACATATATACACATACTATATA 4159

Qy       1500 CATTGTTACTATTTTAGTCACTGAATAATATGGCTT---AATTTGCTTATACATCCTCCT 1556
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Qy       1557 GCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGA 1616
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Qy       1717 AAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAG 1776
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Qy       1777 GTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCT 1836
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Qy       1837 ATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCT 1896
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Qy       1897 ACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAG----TG 1952
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Qy       1953 AGCCGAGATCCCACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAA 2012
Db       3678 TGCTGAGACTGCACTGCTGCCCTCCAGCCTGGGTGACAGAGCAAGACTCCATCCCAAAAG 3619

Qy       2013 AATAAATAAATAAAATAAAGGATCGGAGAGAAACAAAACTAATAAGATTCCTGAAGGTAA 2072
Db       3618 AAAAGTTAAGTAAATAAAATATAAGTTAAGTTCACACATAATCTAACAATTTTTAAATAT 3559

Qy       2073 GCAGAGATACGTAAATTATATGTAATAAAGTTTAAATGCATTTTAACTGTAATCTTATTG 2132
Db       3558 ATTGCATTTTATTACGTAACAGTAAAATTAGTAAAATAATTGATATACTTTAATTTATAA 3499

Qy       2133 TTTATTTTGGTTATAAAAGTAAACAA 2158
Db       3498 TTTCTTTCTCTCAGTATAATGTAGAA 3473
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RESULT 8
CR860521/c
LOCUS CR860521 1605 bp mRNA linear HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp468P2419 (from clone DKFZp468P2419).
ACCESSION CR860521
VERSION CR860521.1 GI:55731876
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE 1 (bases 1 to 1605)
AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
CONSRTM The German cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp468P2419) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468P2419
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

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                     DH10B; sites SfilA + SfilB"
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ORIGIN

  Query Match            12.1%;  Score 301.2;  DB 4;  Length 1605;
  Best Local Similarity  67.7%;  Pred. No. 6.6e-18;
  Matches  474;  Conservative    1;  Mismatches  204;  Indels   21;  Gaps    3;

Qy        598 TTTGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAG 657
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Qy        658 CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTG 717
Db       1542 TGTAGTGGTGCAATCTCAGCTCACTGCAACATCCATCTCCCGGATTCCACTTATTCTCCT 1483

Qy        718 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAA 777
Db       1482 GCCTCAGCCTCTCAGGTAGCTGGGATTATGGGTGCCTGCCATAATGCCCAACTCAATTTT 1423

Qy        778 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGG 837
Db       1422 GTA--CTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGG 1365

Qy        838 CTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACC 897
Db       1364 CCTCAAGTGATCCACCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGACCACTG 1305

Qy        898 ATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAA 957
Db       1304 CACCTGGCCTGAATTTCTCCATTCTTCCCA-----CACACCCGCCTCAGGTTCTCCTTCC 1250

Qy        958 CAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCT 1017
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Qy       1018 CAACCTCCGTTCA--------------GCTCACTGCAACCTCTGCCTCCCGGGTTCAAGY 1063
Db       1189 AGACTGGAGTGCAGTAGTGCAATCTTGGCTCACTGAAACCTCTTCCTCCCAGCCTCAAGC 1130

Qy       1064 GATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGG 1123
Db       1129 GATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGATTACATGTGTGCACCACTAACACCCA 1070

Qy       1124 CTAATTTTTTGTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAA 1183
Db       1069 GATAATTTTTGTACTTTTAGTAGAGATGGGGTTTGACCATATTGGCCAGACTGGTCTTGA 1010

Qy       1184 ACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGT 1243
Db       1009 ATTCCTGACCTCAGGTGATCCGCCCACCTCAGCCTCCCAAAGTGTTGGGGTTATAGGCGT 950

Qy       1244 GAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTAT 1283
Db        949 GAGCCACTGCACCCGGCCCCCTTCCTTCATCTTAGTCAAT 910


RESULT 9
CR599842
LOCUS       CR599842               1863 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DA002YO06 of Neuroblastoma of Homo
            sapiens (human).
ACCESSION   CR599842
VERSION     CR599842.1  GI:50480649
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1863)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1863)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
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                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match            12.1%;  Score 301.2;  DB 4;  Length 1863;
  Best Local Similarity  56.9%;  Pred. No. 6e-18;
  Matches  811;  Conservative    1;  Mismatches  509;  Indels  105;  Gaps   10;

Qy        624 GAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTG 683
Db        496 GGGTCAGAGTCTCACTCTGTTTCCCAGGCTGGAGTTCTGTGGCACCGTGTTGGCTCACTG 555

Qy        684 CAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGAC 743
Db        556 CAACCTCCGTCTCCTGGGTTCAAGCAATTCTCTTGCCTCAGCCTCCAGAGTAGCTGGGAT 615

Qy        744 TACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATTTTTTTGTAGAGACTGGGTCT 803
Db        616 TACAGGTGCCCACCACCACACCCGGCTAATTTTTTTATATTTTTAGTAGACACGGGGTTT 675

Qy        804 TACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCA 863
Db        676 CACCATGTTGGCCAGGCCGGTCTTGAACTTGTGACGTCAGGTGATGCACCCGCCTTGGCC 735

Qy        864 TCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACAT 923
Db        736 TCCCAAAGTGCTGGGATTACAGGTCCAGATTTTGAACAAATCTCGCTAGAGATTGAACAG 795

Qy        924 TCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCCT 983
Db        796 AGCTGCGCCTGGATCCCGCCACAGTGAGGAGACCTGAAGACCAGAGAAAACACAGCAAAC 855

Qy        984 TTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTCAGCTCACTGCAA-C 1042
Db        856 GGAGTCTTGCTCTGTTGTCCAGGCTGGAGTGTAGTGTGGCGATCTCGGCTCCCTGCAAGA 915

Qy       1043 CTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACA 1102
Db        916 ATCTGCCTCCCAGATTCACGCCATTTTCCCACCTCAGCCCCTGGAGTAGCTGGAAGTACA 975

Qy       1103 AGCGTGCACCACCATGCTTGGCTAAT----TTTTTGTATTTTTAGCAGAGATGGGGTTTT 1158
Db        976 GGCTCCCGCCACCACGCCTGGCTAATTTTGTTTTTGTATTTTTAGTAGAGACGGGGTTTC 1035
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Qy       1159 ACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCT 1218
Db       1036 ACTGTGTTAGGTAGGATGGTCTCGATCTCCTGACCTCA--TGATCCATCCGCCTTGGCCT 1093

Qy       1219 CCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTC 1278
Db       1094 CTCAAAGTGCTGGGATTACAGGCATGAGCCACCGCACCTGGCTG------------TTTT 1141

Qy       1279 TTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAAT 1338
Db       1142 TTCATTTCTATTATGATTTGTTCTGTGGAATGTCAGTGACTTAGCGGTGTTTTTCACATG 1201

Qy       1339 AATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCTTTTTTTAAAACAATCTTGA 1398
Db       1202 TTTATAAAGCTGAATAGTTCTGTATGTCAGCTCAGCACCCCTAGTGTCAGTCATGCTACT 1261

Qy       1399 CAACTTTGCAGAATAAATACAATCTTGCATTCTGCTTTTTCACTTATCACCTTGTTATGA 1458
Db       1262 CTCCTGCTGTGCATAGATGGGGGCCTGTCCACACCCAAATCTCCTGGGTTCCCGCTGTCC 1321

Qy       1459 CTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTC 1518
Db       1322 GCACCTGAAGGTACCCACCAGATGTGTCTGTCACTGCCCTCCATCCACCTTTCTTGTGGT 1381

Qy       1519 ACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAAT 1578
Db       1382 TCTCATGTTTCTGCCTC------CCTAGAGACCATTTCTCTCTACAGCAGTAG------- 1428

Qy       1579 TTACAAATCTGATGAAAGCTATGAACCCTCTCCCCAGAGAAATACACACACACACACACA 1638
Db       1429 ----------------------------TTTCCAATAGAAATACAATGCCAGACACATA 1459

Qy       1639 CTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATG 1698
Db       1460 C---------GTCATTTTAGATTTTCTAGTAGTCACTTTAGAAAAGTGAAAAAGAGGCCA 1510

Qy       1699 TTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACA 1758
Db       1511 GCTG--------------------------------CAGTGGCTCACACCTGTAATCCCA 1538

Qy       1759 GTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGG 1818
Db       1539 GCACTTTGGAAGGCTGAGGTGGGTGGATCAC--GAGGTCAGGAGATCGAGACCATCCTGG 1596

Qy       1819 TCAATATGGTGAAACCCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATG 1877
Db       1597 CCAACATGGTGAAACCCCCTCTCTACTAAAAATACAAAAAATTAGCTGGGCGTGGTGGCA 1656

Qy       1878 CATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAG 1937
Db       1657 GGCGCCTGTAGTCCCAGCTACTCGAGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGTAG 1716

Qy       1938 GCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGGCGACACAGCGAG 1997
Db       1717 GCAGAGCTTGCAGTGAGCCGAGATAGCGCCACTGCACTCCAGCCTGGGCGACAGAGGGAG 1776

Qy       1998 ACTCTATCTCAAAAAAATAAATAAATAAAATAAAGGATCGGAGAGA 2043
Db       1777 ACTCCATCTCAAAAAAAAAAAAAAGGTTACAAAGAAACAGGTGAAA 1822
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RESULT 10
BQ958903
LOCUS       BQ958903                946 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_10035485 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6483214
            5', mRNA sequence.
ACCESSION   BQ958903
VERSION     BQ958903.1  GI:22374381
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 946)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2667  row: g  column: 23
            High quality sequence stop: 534.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6483214"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_40"
                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California,  Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life  Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match            12.0%;  Score 300.6;  DB 5;  Length 946;
  Best Local Similarity  69.1%;  Pred. No. 1e-17;
  Matches  468;  Conservative    1;  Mismatches  197;  Indels   11;  Gaps    4;

Qy        596 AGTTTGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATG 655
Db         24 AGNTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTTGCTCTGTCACCCAGGCTGG 83

Qy        656 AGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGC 715
Db         84 AGTGCAGTGGTG---CGATCGCTCACTGCAACCTCAGCCTCCTGGATTTAAGTGATTCTC 140

Qy        716 TGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTA 775
Db        141 CTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGCACCACCATGCCCGGCTAATTT 200

Qy        776 AAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCT 835
Db        201 TTTTGTATTTTTAGTGGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCT 260

Qy        836 GGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCA 895
Db        261 GACCTC--GTGATCCGCCTGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCA 318

Qy        896 CCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAG 955
Db        319 CCACGCCTGGCCCCAGTCCAAAATATTTAAAGATTGTTTCCTTAGTGTCTTGAAGTTTTG 378

Qy        956 AACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCAC 1015
Db        379 CACA-----AAATTCTTTTTTTTGAGATGGAGTCTCACTCTGTCACCCAGGCTGGAGTGC 433

Qy       1016 CTCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCC 1075
Db        434 AGTGGCGTGATCTTGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCAATTCTCCCACC 493

Qy       1076 TAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGT 1135
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Db        494 TCAGCCTCCCAAGTAGCTGGGATTACAGACGTGTGCCACCATACCTGGGTAA-TTTTTGC 552

Qy       1136 ATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTC 1195

Db        553 ATTTTTAGTGGAGAGGGAGTTTCACCATGTTGGCCAGGGTGGTCTTGAACTCCTGACCTC 612

Qy       1196 AAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGC 1255

Db        613 AGGTGATCCTCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGTGC 672

Qy       1256 CTGGCCGATTACTGTCT 1272

Db        673 TCAGCCGCANAATTCCT 689


RESULT 11
BQ706343/c
LOCUS       BQ706343                 918 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8484983 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301091
            5', mRNA sequence.
ACCESSION   BQ706343
VERSION     BQ706343.1  GI:21845242
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 918)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2516  row: g  column: 12
            High quality sequence stop: 632.
FEATURES             Location/Qualifiers
     source          1. .918
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301091"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match            11.9%;  Score 298;  DB 5;  Length 918;
  Best Local Similarity   68.6%;  Pred. No. 1.8e-17;
  Matches  456;  Conservative    1;  Mismatches  197;  Indels   11;  Gaps    3;

Qy        598 TTTGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAG 657

Db        666 TTTTGGATTATGATTATTATTCTTTGAAGCCAGGGTCTCGCTCTGTCACNCAGGCCGGAG 607

Qy        658 CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTG 717

Db        606 TGCAGTGGTGCAATCATGGCTCACTCCAGCCTTTATCTCCTGGGCCCAAGTGATCCTCCA 547

Qy        718 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTA------ 771

Db        546 ACCTCAGCCTCCCAAGTAGCTGGGATTATAAGTGCGTGCTACGATGTCTGGCTAATTTTT 487

Qy        772 -ATTAAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAA 830

Db        486 TATTTATAAATATTTTTTGTAGAGACAGGGTCTCGCTTTGTTGCCCAGGCTGGTCTCAAA 427

Qy        831 CTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTG 890

Db        426 TTCCTGGACTCAGGCGATCCTCCTGCTTCAGCCTCCCAAAGTGCTGAGATTACAGGCGTG 367

Qy        891 AGCC---ACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAG 947

Db        366 AACCTTTCAACTTTTAATGCTTTCAGTATTTTCCCATCCCTTGATTGAACATTTGGGTTT 307

Qy        948 ATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCAC 1007

Db        306 TAAATTATTTTTGTTGTTGTTGTTTCTTTTTGAGACAGAGTCTTGCTCTGTCACCCAGGC 247

Qy       1008 TTCATCACCTCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATT 1067

Db        246 TAGAATGCAGGGGTGTGATCTCGGCTCACTGCAACCTCTGCCTCCTGCGTTCAAGCGATT 187

Qy       1068 CTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAA 1127

Db        186 CTTGTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCGCCTGCCATGATGCCCAACTAA 127

Qy       1128 TTTTTTGTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTC 1187

Db        126 TTTTTTGTATTTTTAGTAGAGACAGTGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTC 67

Qy       1188 CTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCA-AAGTGCTGGAATTATAGGCGTGAG 1246

Db         66 CTGACCTCAAGTGATCCGCGCACCTTGGCCTCCCANAATTGCTGGGATTACAGGTGTGAG 7

Qy       1247 TCACT 1251

Db           6 CCACT 2


RESULT 12
CX780936
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DEFINITION  HESC3_2_B04.b1_A036 NIH_MGC_260 Homo sapiens cDNA clone
            IMAGE:30928759 3', mRNA sequence.
ACCESSION   CX780936
VERSION     CX780936.1  GI:58297726
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: HESC3_2_B04.g1_A036
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: BresaGen, Inc.
             cDNA Library Preparation: Express Genomics, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
            University of Georgia
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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           Plate: NDAM1172  row: c  column: 08
           Seq primer: M13-21 (TGTAAAACGACGGCCAGT)
           High quality sequence stop: 711
           POLYA=Yes.
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     source          1. .736
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                     /mol_type="mRNA"
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                     /clone="IMAGE:30928759"
                     /sex="male"
                     /tissue_type="human embryonic stem cells"
                     /cell_type="human embryonic stem cells"
                     /cell_line="BG01"
                     /lab_host="DH10B-T1 phage-resistant E. coli"
                     /clone_lib="NIH_MGC_260"
                     /note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV;
                     RNA obtained from human embryonic stem cells isolated from
                     the inner cell mass of blastocyst stage embryos. Cell line
                     id and NIH Registry designation is BG01. Positive for
                     SSEA3, SSEA4, Tra 1-60, Tra 1-81, CD9, Alk Phos, Oct4 and
                     Nanog expression; negative for SSEA1 expression. Passage
                     number 21. cDNA primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. This primary library
                     is non-normalized (normalized primary library is
                     NIH_MGC_261). It was constructed by Express Genomics
                     (Frederick, MD). Sequence ends have been trimmed to
                     exclude vector and regions below Phred quality 16. Note:
                     this is a Mammalian Gene Collection library."
ORIGIN

  Query Match             11.7%;  Score 293.6;  DB 8;  Length 736;
  Best Local Similarity   66.9%;  Pred. No. 5e-17;
  Matches  464;  Conservative    1;  Mismatches  220;  Indels    9;  Gaps    3;

Qy        599 TTGGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGC 658
              ||   |||||||||  || || ||| ||||  | ||||  |||| |  |||||||   ||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTCTCACTCTCTTGCCCAGGCTGAAGT 60

Qy        659 ACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGA 718
              ||||||  |   | |    | ||||||||  ||||   |||||||  | |||||    |
Db         61 GCAGTGGCGGGATCTCGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCACTTCTTCTG 120

Qy        719 CCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAA 778
              | |||||| ||  ||||||||||| |||  ||   |||||||| |||||| || ||
Db        121 CTTCAGCCCCCTGAGTAGCTGGGATTACAGGCACCCACCACCAGGCCTGGATACTT--TT 178

Qy        779 AAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGC 838
              | |||||    | | ||||  || |||  |||||||||| |||| |||||||||  |
Db        179 TTGTATTTTTAGTAAAAATGGGGTTTGCTATATTGGCCAGGCTGGTCTCAAACTCCTGAC 238

Qy        839 TTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCA 898
              |||  |  |||| ||| |||   || | ||||||||||||||||||||||  ||| ||||||
Db        239 CTCAGGTGATCCACCTGCCTAAGCCTGCCAAAGTGCTGGGATTACAGGCATGAACCACCA 298

Qy        899 TGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAAC 958
              ||   | ||  |||  ||||||  | ||          ||     | |  |     |
Db        299 TGCCCAGCCTCTTTATTCTTTTTAATATTATCACAAGTTATTTATTTATTTATTTATTTA 358

Qy        959 AGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTC 1018
              |||  |    |     |||     ||   | |  ||     | | ||    | ||
Db        359 TTTATTTATTTTTTGAGATGGAGTTTTGCCCTTGTTGCCCAAGCTGGAGTGCAATGGCAC 418

Qy       1019 AACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAA 1078
              | |     |||||||||||||||||  |||||||||||||||:|||||||||||||| |
Db        419 GATC-----TCAGCTCACTGCAACCTCCACCTCCCGGGTTCAAGTGATTCTCCTGCCTCA 473

Qy       1079 GCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATT 1138
              |||||||||||||||| ||||||  ||      ||| |||||  |||||||   ||||| |||
Db        474 GCCTCCTGAGTAGCTGGGATTACAGGCACATGCCATCATGCCTGGCTAA--TTTTGCATT 531

Qy       1139 TTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAG 1198
              ||||| |||||  | ||||  |||||||  ||||||||||  |||||||||||||| |
Db        532 TTTAGTAGAGACAGAGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGG 591

Qy       1199 TGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTG 1258
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Db        592 TGATCTGCCCTCCTCGGCCTCCCAAAGTGCTGGGATTATAGGCATGAGCCACCGTGCCCA 651

Qy       1259 GCCGATTACTGTCTATTTTCTTTATTGCTATATC 1292
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Db        652 GCCATTATCACAAGTTATTTATACTTCCTTTCTC 685


RESULT 13
CR613629
LOCUS       CR613629               3092 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI039YN19 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR613629
VERSION     CR613629.1  GI:50494436
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3092)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 3092)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="CS0DI039YN19"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             11.6%;  Score 290.6;  DB 4;  Length 3092;
  Best Local Similarity   69.7%;  Pred. No. 3.7e-17;
  Matches  466;  Conservative    1;  Mismatches  190;  Indels   12;  Gaps    5;

Qy        594 ACAGTTTGGGTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCA 653
              | | |||   ||||||||| || || ||| ||||||| ||||||||||||||||||||
Db       1750 AAATTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTTGCTCTGTCACCCAGGCT 1809

Qy        654 TGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCT 713
              |||  ||||||||    | || | |||||||| ||||| |||||||    | ||| |||
Db       1810 GGAGTGCAGTGGTG---CGATCGCTCACTGCAACCTCAGCCTCCTGGATTTAAGTGATTC 1866

Qy        714 GCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAAT 773
              |    |||||||||||||||||||||||||||| |||  | ||||||||||| ||| |||||||
Db       1867 TCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGCACCACCATGCCCGGCTAAT 1926

Qy        774 TAAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTC 833
              |      | ||||| || ||||| |||| | || | |||||||||||| ||||  |||||
Db       1927 TTTTTGTA-TTTTTAGTGGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTC 1985
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Qy        834 CTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGC 893
              ||| | ||  |  |||| ||| |||  || ||||||||||||||||||||||| ||||||
Db       1986 CTGACCTC--GTGATCCGCCTGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGC 2043

Qy        894 CACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCAC 953
              ||||| |   |||  |          ||  |      | |    |          ||
Db       2044 CACCACGCCTGGCCCCAGTCCAAAATATTTAAAGATTGTTTCCTTAGTGTCTTGAAGTTT 2103

Qy        954 AGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATC 1013
              | |||      | | | | ||||     |    | |         |  |   ||  |
Db       2104 TGCACA-----AAATTCTTTTTTTTGAGATGGAGTCTCACTCTGTCACCCAGGCTGGAGT 2158

Qy       1014 ACCTCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTG 1073
              |      | |     |||||||||||||||||||||| |||||||||: |||||||
Db       2159 GCAGTGGCGTGATCTTGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCAATTCTCCCA 2218

Qy       1074 CCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTT 1133
              ||| |||||||  |||||||| |||||  ||||  |||||| | ||| ||| |||||
Db       2219 CCTCAGCCTCCCAAGTAGCTGGGATTACAGACGTGTGCCACCATACCTGGGTAA-TTTTT 2277

Qy       1134 GTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACC 1193
              | ||||||||  |||| || |||| |||||||| ||||| ||||||  ||||||||||
Db       2278 GCATTTTTAGTGGAGAGGGAGTTTCACCATGTTGGCCAGGTTGGTCTTGAACTCCTGACC 2337

Qy       1194 TCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGT 1253
              ||| ||||||  |||||||| | ||||||||||||||| |||| |||| |||| || ||
Db       2338 TCAGGTGATCCTCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGT 2397

Qy       1254 GCCTGGCCG 1262
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Db       2398 GCTCAGCCG 2406
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RESULT 14
BQ681302/c
LOCUS       BQ681302                 855 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8034339 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6213772
            5', mRNA sequence.
ACCESSION   BQ681302
VERSION     BQ681302.1  GI:21793981
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2380  row: a  column: 05
            High quality sequence stop: 649.
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                     /clone="IMAGE:6213772"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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  Query Match            11.5%;  Score 288.2;  DB 5;  Length 855;
  Best Local Similarity  69.2%;  Pred. No. 1.3e-16;
  Matches  471;  Conservative    1;  Mismatches  161;  Indels   48;  Gaps    4;

Qy        606 TTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTGG 665
              ||||||| || || |||  |||||||||||||| ||||||||||||  |  |||  ||||||
Db        855 TTTTTTTTTTTTTTTTTTTAGACAGGGTCTTGATCTGTCACCCAGACTGGAGTGCAGTGG 796

Qy        666 TGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGC 725
              ||  | ||||| |||||| | | |||| ||| |  ||||| |  ||       || |||||
Db        795 TGAGATCATAGCTCACTGTAACNTCAAACTCTTCGGCTCAGGCAATACTTCCACTTCAGC 736

Qy        726 CTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATTTT 785
              |||||| |||||||||||||| || |     ||||||  ||  ||||| |     || |||
Db        735 TTCCCAAATAGCTGGGACTACAAGTGCATGCCACCATACCCAGCTAAAT-GTTTAAGTTT 677

Qy        786 TTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGC 845
              ||||||||||  |||||||  | | |||   ||||||  ||||||||||||||||||||
Db        676 TTTGTAGAGATGGGGTCTTGCCATGTTTCNCAGGCTGCTCTTAAACTCCTGGCTTCAAGT 617

Qy        846 AATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGG 905
              |||||||  ||||   || ||||||||||||||||  |||||  |||||  |||  |||   ||
Db        616 GATCCTCCCACCTCAGCCTCCCAAAGTGCTGGGATGACAGGTGTGAGACACAATGCCTGG 557

Qy        906 CTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGATT 965
              || ||    |   |  |  |   | ||||  | | |  ||
Db        556 CTTCTCTCTCTCTCTCTTTTTTTTTCTGAAACAGAGT---------------------- 518

Qy        966 ACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCTCC 1025
                          ||| || ||   | |   |  || | ||    ||| |
Db        517 -----------------TTTGTTCTTGTTGCCCAGGCTGCAGTGCAATGGCTCGA----- 480

Qy       1026 GTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCT 1085
              |||||||||||||||||||| ||||||||||||||:|||||||||||||| |||||||
Db        479 TTTCAGCTCACTGCAACCTCTACCTCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCC 420

Qy       1086 GAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAA----TTTTTTGTATTTTT 1141
              ||||||||| |||||| |||    |||||| || ||||| |    ||||||||||||||
Db        419 AAGTAGCTGGGATTACAGGCGCCTGCCACCACGCCTGGCTGACTTTTTTTTTGTATTTTT 360

Qy       1142 AGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA 1201
              || |||||||||||||| |||||| || ||||||||  ||  |||||||||| |||| ||||
Db        359 AGTAGAGATGGGGTTTCACCATGGTGGCCAGGCTGACCTTGAACTCCTGATCTCAGGTGA 300

Qy       1202 TCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCC 1261
              ||  ||  |||  | |||||||||||||||| |||| ||| |||||  |||||||| ||||
Db        299 TCCACCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACTGTGCCCGGCC 240

Qy       1262 GATTACTGTCTATTTTCTTTA 1282
                | ||  |  | ||  | |
Db        239 AGCTTCTTGCCTTCTTACTGA 219
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RESULT 15
BQ710315/c
LOCUS       BQ710315                 769 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8351732 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282212
            5', mRNA sequence.
ACCESSION   BQ710315
VERSION     BQ710315.1  GI:21849214
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
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REFERENCE   1  (bases 1 to 769)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2476  row: d  column: 21
            High quality sequence stop: 549.
FEATURES             Location/Qualifiers
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                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match           11.5%;  Score 287.6;  DB 5;  Length 769;
  Best Local Similarity   67.0%;  Pred. No. 1.6e-16;
  Matches  453;  Conservative    1;  Mismatches  215;  Indels    7;  Gaps    3;

Qy        604 TTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGT 663
              ||||||||| || || | | ||||||| ||||  ||||||| |||||||  |||  ||||
Db        768 TTTTTTTTTTTTTTTTTATTGAGACAGAGTCTCACTCTGTCCCCCAGGCTGGAGTGCAGT 709

Qy        664 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 723
              || |  | |   | |||||||| ||||  ||||||| | |||||  |||   |   |||||
Db        708 GGGGTGATCTCGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCA 649

Qy        724 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCCTGGCTAATTAAAAAAATT 783
              ||||||| ||||||||||||||    |||  | ||||   |||  |   | ||  | |   |
Db        648 GCCTCCCGAGTAGCTGGGACTATAGGCGCCCGCCACTGTGCCGGCTAATTTTTATA---T 592

Qy        784 TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAA 843
              |||| |||||||| |||| |  | | |||||||||||||| ||||  || ||||  | |||
Db        591 TTTTAGTAGAGACGGGGTTTCCCCATGTTGGCCAGGCTGGTCTCGAATTCCTAACCTCAG 532

Qy        844 GCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 903
              |  |||| |||  ||  || ||||||  |||||||||||||| ||||||||||||  |
Db        531 GTGATCCGCCTGGCTCAGCCTCCCAACATGCTGGGATTACAGGTGTGAGCCACCATGCCC 472

Qy        904 GGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGA 963
              ||||   |   ||||   |   |||  |   |          | | ||     |
Db        471 GGCTGTGTTACACTTTTTGTGGTGTCTCACAGGTCTCTGAGGCTCTGCTCATTTTTGTTT 412

Qy        964 TTACTGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCT 1023
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Db        411 TTGTTTTTATTTTTTTGAGACAGAGTCTCTTTCTGTCACTAGACTGGAGTGCAGTGGTGC 352

Qy       1024 CCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTC 1083
                || |||||||||||||||||||||| | |||||||:|||||||| ||||| ||||||
Db        351 AATCTCGGCTCACTGCAACCTCTGCCTCCAGAGTTCAAGCGATTCTCTTGCCTCAGCCTC 292

Qy       1084 CTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAA--TTTTTTGTATTTTT 1141
              |  |||||||| |||||| ||     |||||||||     ||||  ||||||||||||||
Db        291 CCAAGTAGCTGGGATTACAGGCACATGCCACCATGCCCAACTAATTTTTTTTGTATTTTT 232

Qy       1142 AGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA 1201
              || |||||||||||||| |||||||||| ||||| ||||||   | ||| |||||||  ||||
Db        231 AGTAGAGATGGGGTTTGACCATGTTGGCCAGGATGGTCTAGATCTCTTGACCTC--GTGA 174

Qy       1202 TCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCC 1261
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Db        173 TCCAACCACCTTGGCCTCCCAAAGTGCTGAGATTACAGGCGTGAGCCACTGCGCCTGGCC 114

Qy       1262 GATTACTGTCTATTTT 1277
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Db        113 GGCTCCTCCTTCTTAT 98


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